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Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw mciel
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Published_Applications NA New:*

1: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:*

2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq:*

6: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1:*

7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1:*

9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*

10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3:*

11: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

12: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

13: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

14: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

15: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

16: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

17: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

18: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

19: /SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*

19: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
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Gapop 10.0 , Gapext 1.0
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597
1 aacacgagcctgttgacgcc......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  April 7, 2006, 02,41:57; Search time 225.02 Seconds (without alignments)
10613.880 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9267905 seqs, 2000278028 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aacacgagcctgttgacgcc.....cacgaacgcgcagcggggcgc 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.

Result	Score	Query Match	Query Match Length DB	DB	ID	Description
c 1	48.4	8.1	1685	۲ i	US-11-096-568A-22628	Sequence 22628, A
ი 2	46.8	7.8	1092	œ	US-10-467-657-4105	Sequence 4105, Ap
ω	43.2	7.2	1773	1	US-11-096-568A-22025	Sequence 22025, A
0 4	42	7.0	1986	ä	US-11-096-568A-17491	Sequence 17491, A
ი 5	41.8	7.0	1147	1	US-11-096-568A-26890	Sequence 26890, A
ი ი	41.8	7.0	1444	11	US-11-096-568A-20988	Sequence 20988, A
c 7	41.8	7.0	2506	11	US-11-096-568A-19863	Sequence 19863, A
ი 8	41.2	6.9	1492	H	US-11-096-568A-10536	Sequence 10536, A
ø	40.4	6.8	11070	14	US-11-075-185-34	Sequence 34, Appl
10	40.4	6.8	78869	14	US-11-075-185-1	Sequence 1, Appli
c 11	40	6.7	1340	H	US-11-096-568A-19408	Sequence 19408, A
c 12	39.6	6.6	1284	9	US-10-714-887-121	Sequence 121, App
c 13	39.4	6.6	1416	œ	US-10-858-730-195	Sequence 195, App
C 14	39.4	6.6	1694969	7	US-10-506-454-1690	Sequence 1690, Ap
c 15	39.2	6.6	806	11	US-11-096-568A-5433	Sequence 5433, Ap
16	39	6.5	1591	11	US-11-096-568A-19813	Sequence 19813, A
c 17	39	6.5	88421	14	US-11-205-109-1	Sequence 1, Appli
18	38.2	6.4	1216	8	US-10-821-234-838	Sequence 838, App

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36.1	36.8	36.	ų	37	37.	37.	37.	37.	37.2	37.2	37.	37.2	37.4	37.4	37.	37.	37.	37.8	37.	37.8	37.8	37.8	37.8	38	38	ω
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2078	1264	1247	1296	765	170189	161726	161726	157224	3342	1328	1212	1096	355211	1629	1187	2124	1022	78869	5301	4185	3017	1435	1095	3513	3408	849
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US-11-024-959-52	11-0	·11-0	·11-0	0-71	·11-1	·11-1	·11-1	·11-1	·11-1	·11-0	·11-0	10-71	10-33	10-50	·11-0	.11-0	-11-0	-11-0	-11-0	LO-79	10-79	-11-0	10-79	10-85	L0-85	·11-0
24-9	US-11-096-568A-23146	US-11-096-568A-10198	US-11-096-568A-23788	US-10-714-887-125	US-11-112-908-50	US-11-112-908-52	112-908-48	112-908-51	US-11-169-041-95	US-11-096-568A-8975	<b>US-11-000-688-63</b>	US-10-714-887-117	US-10-330-773-242	US-10-501-035-167	US-11-096-568A-22600	US-11-096-568A-23989	US-11-096-568A-10781	US-11-075-185-1	US-11-075-185-40	US-10-793-626-3646	US-10-793-626-4422	US-11-096-568A-11892	US-10-793-626-307	US-10-858-730-142	US-10-858-730-40	US-11-096-568A-21222
59-52	58A-2	58A-1	58A-2	7-125	08-50	<b>08-52</b>	08-48	08-51	11-95	58A-8	38-63	7-117	3-242	5-167	58A-2	58A-2	58A-1	35-1	85-40	6-364	5-442	58A-1	5-307	0-142	0-40	68A-2
••	3146	0198	3788	•	_		_		•	975	ű				2600	3989	.0781		_	õ	ί	1892	์ ज			1222
Seq	Seq	Seg	Seg	Sequ	Seq	Seg	Seg	Seg	Seq	Seq	Seq	Sequ	Sequ	Sequ	Seg	Seq	Seg	Seg	Seq	Sequ	Sequ	Seq	Sequ	Sequ	Sequ	Seq
Sequence	Sequence	Sequence	Sequence 23788, A	Sequence 125, App	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 8975, Ap	Sequence 635	Sequence 117,	Sequence 242,	Sequence 167,	Sequence 22600,	Sequence 23989	Sequence	Sequence 1, Appli	Sequence 40,	Sequence 3646	Sequence 4422, Ap	Sequence 11892, A	Sequence	Sequence	Sequence 40,	Sequence 21222,
		9 10	e 23:	125					e 95,	99.	e 63!	117	242	167	e 22	e 23	e 10.	1	9 40	364	442	e 11	3075	142	4 0,	e 21:
52, Appl	23146,	10198,	788,	Apr		Appl			Appl	75, 7	5, App	Apr	Apr	, App	60	989,	10781,	Appl	, Appl	Ap	2, Ar	392,	ς, Αρ	, App	Appl	222,
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### ALIGNMENTS

P	β	용	Ş	皮	Ş	유 상	Query M Best Lo Matches	WS-11-096- Sequence Publicat: GENERAL: APPLICAN: APPLICAN: TITLE OI TITLE OI TITLE OI TITLE OI TITLE OI TITLE OI TITLE OI FILB REI CURRENT CURRENT CURRENT CURRENT NUMBER (A SEQ ID NV SEQ ID NV SEQ ID NV SEQ ID NO SEQ ID	
753 ACGTCATGAGCGCCTGCGTCCGGCCCGGTGGTCGGGCGTCCAGTACACGGTGGACGGCA 694	203 CGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGACTGCGCTCGGCGAGGGTCGACG 262	813 AGACGCAGCAGGACGGGTACCGGGGACGCCAGCTGCTGCGAGTAGGTGCAGGTCACCGTCC 754	143 CGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCT 202	873 CGCAGCCGCACCGGGCGCACCGCACGGTGCTGTTGTAGAAGGAGGAGAAGG 814	83 CGCGGCCCGACAGAACTGGCACGCAAGGCGCACCCCGCCTGAGACGAGACGCAGG 142	23 GCCCGAGCGCCACCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCCTTGAGGCCGT 82	Query Match 8.1%; Score 48.4; DB 11; Length 1685; Best Local Similarity 47.0%; Pred. No. 0.00058; Matches 185; Conservative 0; Mismatches 206; Indels 3; Gaps 1;	US-11-096-568A-22628/c US-11-096-568A-22628/c Sequence 22628, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION: APPLICATION: APPLICATION: Sequence-Determined DNA Fragments and Corresponding Polypeptide TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 22628 LENGTH: 1685 TYPE: DNA CORANISM: Zea mays subsp. mays FEATURE: NAME/KEY: misc_feature LOCATION: (1): 7[1685) TOTHER INFORMATION: Ceres Seq. ID no. 12409422 US-11-096-568A-22628	

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US-10-467-657-4105/c
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US-11-096-568A-22025
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Best Local S
Matches 99
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Publication No. US20050260581A1
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SEQ ID NO 4105
LENGTH: 1092
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                                                                                                                                                         Sequence 22025, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 22025
LENGTH: 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHIRON SPA
APPLICANT: PONTANA MARÍA RÍTA
APPLICANT: PIZZA MARÍAGRAZÍA
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                  APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DN
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: GB-0103424.8 PRIOR FILING DATE: 2001-02-12
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                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                   354 ACAAAATGTACATTCCAAAGCGCAGCCGACTTGCGAGGAAATGCAGAGCGTGCCGCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACGGCGGCGGCCCGCAGGTGTAGCCCAGGCCCCATGAGCGTGAAGTTCCTGG 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC
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53.2%;
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Pred. No. 0.0016;
0; Mismatches 8
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TYPE: DNA
GRANISM: Zea mays subsp. m
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1986)
OTHER INFORMATION: Ceres Se
US-11-096-568A-17491
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US-11-096-568A-17491/c
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APPLICANT: Alexandrov, Nickolai et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17491, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 17491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%;
Best Local Similarity 54.0%;
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                               Matches 135;
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592FUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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NAME/KEY: misc feature

'COATION: (1742)...(174

'TON: n i
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LOCATION: (1767)..(1767)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is
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125 CCTGAGACGAGGCGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGA
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                                            CGGCGCCGGGGAGGCCCAGCCGAGCACGCTGACGAACAGGTAGTTGAGGAGGCACAGG
                                                                        CGATGATGTAGACGACCTGGCCGAGCGCGATGATCCAGTGCGCGATGTCGTAGGCGGCGG
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46.6%;
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                                                                                                                                                              Score 42; DB 11; L
Pred. No. 0.038;
0; Mismatches 155;
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Pred. No. 0.017;
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RESULT 6
US-11-096-568A-20988/c
US-11-096-568A-20988/c
; Sequence 20988, Application US/11096568A
; Publication No. US20060048240A1
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides |
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; LOCATION: (1)..(1147)
; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-26890
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US-11-096-568A-26890/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26890, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alexandrov, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676 AACTCGATACCATAGGAGAGGTGGGTGATGGCGACGTCGTCGAGGATGATGTTGAACTCG
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                                                                                                                                                                                                                                      GGCACGAGGAAATGGGTGCCCTCGCCGACGGTCTCCGGGAGCACC
                                                                                                                                                                                                                                                                                                                                                     TGGGCCGAGTCTTTGCGCTGCCGATAAAGCTTGTCGAAGATGTCGGCTGCCTTTGCCGTTCG
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                                                                                                                                                                                                                                                                               CCGCCGACGCGCCCCGAGCTCGGAGAACGACAGGTCGAAGACC
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Pred. No. 0.042;
0; Mismatches 2
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20988
LENGTH: 1444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(1444)
OTHER INFORMATION: Ceres Seq. ID no. 12391561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays subsp.
FEATURE:
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 687 GTTGCCGATGAAGTGGG
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                              TAGACCCACGACCTGGG
                                                                                                    GAGCTCGGAGAACGACAGGTCGAAGACCGGACGGCGACGGGTCGTCGTCGCCGAATGGG
                                                                                                                                                                                                                                                                              CATGCGCGTGACGGAGAGCCCCGGGAGGGCCCTTGGACGCCCCAGCGCGCGTTCTTGACGGC
                                                                                                                                                                                                                                                                                                             GACCAGCTCGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGACTGCGCTCGGCGAG 254
                                                                                                                                                                                                                                                                                                                                                 GGCGTTGGCGGAGATGGCGAAGACGCCGTCCAGCTCCACCATGACGGTGTTGACGGCGTC
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                                                                    GACGAAGGTGACCCCCAGCGCTGCACCCACGTGAAGTCGCGGTTGAGGGCCCGGGTTGTG
                                                                                                                                        CIGCCGATAAAGCTIGTCGAAAGAIGTCGGCTGCCTTGCCGTTCGCCGCCGACGCGCTCCGC
                                                                                                                                                                                                          GTCGACGTCGACGGGCTCGGCGTCCAAGGTGAGCTGGATGTGGTCGTCCTCCTCCTCCCA
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43.5%;
671
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Pred. No. 0.042;
0; Mismatches 247;
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Sequence 19863, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19863
LENGTH: 2506
TYPE: DNA
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2506)
TOTHER INFORMATION: Ceres Seq. ID no. 12375134
US-11-096-568A-19863
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US-11-096-568A-19863/c

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RESULT 8

US-11-096-56BA-10536/c

US-11-096-56BA-10536, Application US/1109656BA

Publication No. US20060048240A1

GENERAL IMFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Cor

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592FUS2

CURRENT APPLICATION NUMBER: US/11/096,56BA

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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Best Local Simi
Matches 139;
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Best Local S
Matches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 10536
LENGTH: 1492
                                                                                                                                                                                                                                                                                                                                LOCATION: (1). (1492)
OTHER INFORMATION: Ceres Seq.
-11-096-568A-10536
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (1)..(1492)
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                     Local Similarity
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39; Conservative
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   CTCGGCGAGGGTCGACGAGAGG 267
                                                           ATTGCCGTCGACCAGCTCGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGACTGCG
                                                                                                                                                      GGCGCGCCCGTTCACCTTGATGGCCGTCACGCCGATGAAGTACTCGTTCGACTTGTCCTT
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                                                                                                                                                                                                              GAGCCTGTTGACGCCGGGCCCGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGTAGCAG
                               CTTGGAGAGGTCCACCCCGGGCTGGAACGCGTAGGGCGCGTCGCCGAAGACGACGGCCCC
                                                                                          CTCGCCGGAGACGCCGGCGGTGCTCACGTTGTTGACGAGCAGCGGGGTGTAGAGGAGCGA
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ilarity 47.3%;
Conservative
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Pred. No. 0.043;
0; Mismatches 162;
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Pred. No. 0.063;
0; Mismatches 138;
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Sequence 1, Application US/11075185

Publication No. US20050266434A1

GENERAL INFORMATION:
APPLICANT: RESUES, CHRISTOPHER D
APPLICANT: JULIEN, BRYAN
APPLICANT: REID, RALPH
ITITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FO)
FILE REFERENCE: 010099.03

CURRENT APPLICATION NUMBER: US/11/075,185

CURRENT FILING DATE: 2005-03-07
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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-34
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US-11-075-185-34
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US-11-075-185-1
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Publication No. US20050266434A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION UNMER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
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APPLICANT: JULIEN, BRYAN
APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER
FILE REFERENCE: 010099.03
                                                                                                                                                                                                                                                                                                                                                   8246 TGGCGGCGCGCTCGGTGCACGCGCGGTGGCGGGGCTGCCCGAGCTGCTCGCGTCGCTGC 8305
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TGGCGGCGCGCAGCTGGCGGCGACGGAGCTCGTCGTCGTGACGCGCGGCGCGGTGGCGG
                                                       TTGCGCTGCCGATAAAGCTTGTCGAAGATGTCGGCTGCTTTGCCGTTCGCCGACGCGACGCGC
                                                                                                                 CGGTCGTCGACGCCGTGCACGCCGCGCGCGCGCGCGCTGTCCCTGGTGCAGGGGTGGC
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Pred. No. 0.11;
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US-11-096-568A-19408/c
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                                                                                                                                Query Match
Best Local Similarity
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                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Sequence-Determined DNF
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)..(1340)
OTHER INFORMATION: Cert
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ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTGGACGACACGGCGTTTGTGCCGGAGGAGCACGTCGTCGGCGGCGGCGACGGCGCGC 12446
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                                                                                                                                       6.7%;
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                                                                                                     Score 40; DB 1:
Pred. No. 0.14;
0; Mismatches
                                                                                                                                                                                                                                                                           ID no.
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                                                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14;
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                                                                                                                                                                     Length 1340;
                                                                                                     Indels
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; ORGANISM: Oryza sativa (japonica cultivar-group)
; FEATURE:
; OTHER INFORMATION: G3690 Predicted polypeptide sequence is orthologous to G2999
US-10-714-887-121
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US-10-714-887-121/c
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                                                                                                                   Remaining Prior Application data
NUMBER OF SEQ ID NOS: 430
SOFTWARE: PatentIn version 3.2
SEQ ID NO 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121, Application US/10714887 Publication No. US20060015972A1
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                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 10/412,699
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/135,134
PRIOR FILING DATE: 1999-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHERMAN, Bradley K
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MBI0058-CIP
CURRENT APPLICATION NUMBER: US/10/714,887
CURRENT FILING DATE: 2003-11-13
                                                                                                                                                                                                        PRIOR FILING DATE: 2000-11-16
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/394,519
FILING DATE: 1999-09-13
APPLICATION NUMBER: 09/533,392
                                                                                                                                                                                                                       FILING DATE: 1999-03-23
APPLICATION NUMBER: 09/713,994
                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/125,814
                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/533,030
                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/532,591
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/533,029
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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RIECHMANN, Jose Lui
CREELMAN, Robert
RATCLIFFE, Oliver
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REPETTI, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REUBER, T. Lyni
PINEDA, Omaira
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Query Match Best Local Similarity

6.6%;

Score 39.6; DB 9; Pred. No. 0.18;

Length 1284;

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RESULT 13
US-10-858-730-195/c
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PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PastSEQ for Windows Version 4.
SEQ ID NO 195
LENGTH: 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 195, Application US/10858730
                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
APPLICANT: Driggers, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YOTGEY, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR FILING DATE: 2003-05-30
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Thermobifida fusca
                                                                                                                                                                      1074
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              CGGCGCGAC 413
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                                                                                                                                                                                                                                    GGTCAACGGCGCGTGGGCGTAGCCGGCGGCGACCCCGTTGAACACCCACGCGTCCGGCTC
                                             GCCGTACATGCCGTTGCCGATGTGCAGCATGGGCGAGGTCGAACAGTGGTACACCCA
                                                                            TGCTTGCCGTTCGCCGCCGACGCGCTCCGCGAGCTCGAGACGACACGTCGAAGACCGA
                                                                                                          GTGCTTCAGCGTGTGGGCCGAGTCTTTGCGCTGCCGATAAAGCTTGTCGAAGATGTCGGC 344
                                                                                                                                                                        ACCCGCCCGCATCCGGGCGACCTGGTCGGCCGGCTGCCCGGCTCGCCCAGGTACAGCTCTCC 1015
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O'Leary, Jessica
O'Toole, George
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Walbridge, Michael J.
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                                                                                                                                                                                                                                                                                                                             Score 39.4;
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; ORGANISM: Methanopyrus kandleri
US-10-506-454-1690
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                                           US-11-096-568A-5433
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APPLICANT: Mezhevag, Katj
APPLICANT: Polushin, Nikola
APPLICANT: Shcherbinina, O
APPLICANT: Shakhova, Vera V
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5433, Application US/11096568A Publication No. US20060048240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mezhevaya, Katja V
APPLICANT: Polushin, Nikolai N
APPLICANT: Shcherbinina, Olga V
APPLICANT: Shchova, Vera V
APPLICANT: Shakhova, Vera V
APPLICANT: Malykh, Andrei G
APPLICANT: Kozyavkin, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and
TITLE OF INVENTION: and Methods of Use Thereof
FILE DEFENDENCE. FILES
                                                                                                                                                                                                                                 SEQ ID NO 5433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/506,454
CURRENT FILLING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: PCT/US03/06664
PRIOR FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 34471
                                                                   LOCATION: (1). (908 OTHER INFORMATION:
                                                                                                                                 TYPE: DNA
ORGANISM: Glycine max
FEATURE:
                                                                                      NAME/KEY: misc_feature LOCATION: (1)..(908)
                                                                                                                                                                                                      LENGTH: 908
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6.6%;
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Pred. No. 0.25;
0; Mismatches
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7, 2006, 03:50:18	411 GAACTCGGCGAGGCAGATGGCGCACTCG 384	CAGCTCGAACAGGAACTTTGTCGTCTGG 225	AACG	CCGT	ceco	GACG	Best Local Similarity 54.1%; Pred. No. 0.23; Matches 80; Conservative 0; Mismatches
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			AGCAC	ACCGI	GAGTO	78 GCCGTCGCCGGCCGACGCGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGAC	, 68;
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CF429132	CN150225	CF432927	CN151959	AW924660	CF432914	BM322439	CK124607	CD922535	BE415712	CK152637	BF265573	CV948570	CV948578	BI955767	DR741095	CNS0091P	CK152875	вн899909	CK151489	CL685281	CN026633	ID
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7.9	7.9	7.9	7.9	7.9	7.9	7.9	8.1	8.1	8.1	8.1	8.1	æ ω	8.4	8.4	8.4	8.4	æ.5	æ.5	8.6	8.7	8.7	8.7
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CC637331	BG310173	C0093637	CC678957	CA195481	DR807853	DR800406	CB213001	CC668550	BZ529589	BZ529592	CG381651	CN026914	CA085330	CD233416	CD233402	CD233094	CN027260	CN026960	CNS0091P	CD432831	CN140012	CN142245
CC637331 OGWCX32TH	BG310173 HVSMEc001	CO093637 GR Ea15F	CC678957 OGWHG92TH	CA195481 SCEZSB109	DR807853 ZM BFb003	DR800406 ZM_BFb002	CB213001 OML03281	CC668550 OGUCA72TV	BZ529589 OGAJR36TC	BZ529592 OGAJR36TM	CG381651 OGVDJ78TH	CN026914 UMC-p4civ	CA085330 SCJLAM209	CD233416 SS1_13_B0	CD233402 SS1_13_C0	CD233094 SS1_11_H1	CN027260 UMC-p4civ	CN026960 UMC-p4civ	AL053013 Drosophil	CD432831 ETH1 33 G	CN140012 OX1 33 B0	CN142245 WOUND1 4

## ALIGNMENTS

FEATURES BOUTCE	REFERENCE AUTHORS TITLE JOURNAL PURNED COMMENT	RESULT 1 CNO26633 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
University of Missouri-Columbia M616 Medical Sciences Bldg., Columbia, MO 65212, USA Tel: (573)882-0428 Fax: (573)884-5552 Email: porcine@rnet.missouri.edu POLYA=Yes. Location/Qualifiers 1188	Sus.  1 (bases 1 to 188)  Whitworth, K., Springer, G.K., Forrester, L.J., Spollen, W.G., Ries, J.,  Lamberson, W.R., Bivens, N., Murphy, C.N., Mathialigan, N., Green, J.A.  and Prather, R.S.  Developmental expression of 2489 gene clusters during pig embryogenesis: an expressed sequence tag project  Biol. Reprod. 71 (4), 1230-1243 (2004)  15175238  Contact: DNA Core Facility (Swine Project)	CN026633  CN026633  (mRNA sequence. CN026633  CN026633.1 GI:48721169  EST. Sus scrofa (pig) Sus scrofa Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,

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SOURCE
ORGANISM
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                       Neodiplogasteridae, Pristionchus.
1 (bases 1 to 773)
Srinivasan, J., Otto, G.W., Kahlow,
                                                                                                                                                                                                                                                                      SS
                                                                                                                                                                                                                                                                                                                                            survey sequence.
CL685281
                                                                                                                                                                                                                                                                                                                                                                                                              CL685281 773 bp DNA linear GSS 09-JUL-20: PRI0140d_C01_2 - PRI0140d.BR (773) Mixed stage fosmid library of pacificus var. California Pristionchus pacificus genomic, genomic
                                                                                                                                        Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                                                                                                                                                                                                                           Pristionchus pacificus
                                                                                                                                                                                                                                                                                                     CL685281.1 GI:50193428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGTCG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTGACCGATGATCTCGCCAGTGCTCAAATTGCGCGAGAAACCCTGCTTGCCGGTCGAA 85
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POCCIMENTAL MISSOURI-4-Cell-Embryo-(invivo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (PCR Protocol): The amount of mRNA
that was recovered from occytes and embryos was quite
limiting and was not sufficient for library production
with a standard protocol. Therefore, PCR-based protocol
was utilized for producing libraries. Poly-A RNA was
isolated by using the MicroPoly(A) Pure kit from Ambion
(cat. #1918). The mRNA was reverse transcribed with a
NotI-tag-dTls oligonucleotide and a SMART oligonucleotide
(Clontech) modified to contain a SalI site to generate
full-length cDNA with a sequence complementary to the
SMART oligonucleotide. Sequences within the SMART and dT
oligonucleotides were used as primers to amplify the cDNAs
by PCR with pfu turbo polymerase (Stratagene). The
resulting PCR products were purified, digested with NotI
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Pred. No. 6.7e-05;
D; Mismatches 63
Kahlow, U., Geisler, R. and Sommer, R. for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
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ibrary of P.
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REFERENCE AUTHORS TITLE

AppaDB: an AcedB database

KEYWORDS VERSION ACCESSION RESULT 2 CL685281 LOCUS

DEFINITION

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JOURNAL
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COMMENT
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AUTHORS
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                                                                                                                                                                                            1 (bases 1 to 883)
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gangenswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.
Functional Genomics of Abiotic Stress In Wheat and Canola (Unpublished (2003)
Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evolutionary Biology
Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371
                                                                                Bioinformatics
University of Saskatchewan, Department of Con
1C101 Engineering Building, 57 Campus Drive,
Saskatchewan, S7N SA9, Canada
Tel: 306 966 1769
Pax: 306 966 2033
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in identification of the high quality insert the software Lucy
                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CK151489 883 bp
FGAS034056 Triticum aestivum FGAS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                             Email: fgas_ests@cs.usask.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (bread wheat)
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Similarity 59.3%;
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/clone_lib="Mixed_stage
var. California"
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/mol_type="genomic DNA"
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Pred. No. 0.0012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH899909 561 bp DNA linear GSS 30-AUG-2002 Ot800976 Ostreococcus tauri genomic shotgun library Ostreococcus tauri genomic clone ota04c05.g 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 561)
Derelle, E., Ferraz, C.,
Sabau, X., Courties, C.,
Moreau, H.
                                                                                                                                                       BP 44, Avenue Fontaule, 
Tel: (33)468887309
                                                                                                                                                                                                                 Laboratoire Arago
                                                                                                                                                                                                                                        Contact: Moreau
                                                                                                                                                                                                                                                            J. Phycol. 38 (6),
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Mamiellacese; Ostreococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ostreococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH899909.1
                                                                 Class: shotgun.
                                                                                   Seq primer: reverse
                                                                                                     Email: h.moreau@obs-banyuls.fr
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                                                                                                                                                                                                                                                                                                     (Chlorophytae,
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                                                                                                                                                                                                                                                                                                   libraries for sequencing the genome of Ostreococcus tauri
orophytae, Prasinophyceae): the smallest free-living euka
                                                                                                                                                                                               UMR 7628
                                                                                                                                (33) 468887398
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/note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype CI14106 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Nitro-pyrole_hardened at 2 C for 1 day (24 H) (driver).
organism="Ostreococcus tauri"
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                                      Location/Qualifiers
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/db xref="taxon:4565"
/lab_host="DH5 alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
                                                                                                                                                                                                                                                                                                                                                            University of Saskatchewan, De
IC101 Engineering Building, 57
Saskatchewan, S7N SA9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allard, F., Crosby, W.L., Danyluk, J., Budes, P., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, P. Functional Genomics of Abiotic Stress In Wheat and Canola Crops
                                                                                                                                                                                                                                                      This sequence is the direct result of the Phred (default parameters). It is the raw identification of the high quality insert (default parameters) has been run on this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CK152875
CK152875.1 GI:38972365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGAS035952 Triticum aestivum mRNA sequence.
                                                                                                                                                                                                                                                                                                                                            Email: fgas_ests@cs.usask.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCAACTCTAGCACCTGCGACACGATCTCACTCGCCGAGAGGTTCCGCTTGAAGCCTTG 470
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                                                                                                                                                                                                                                   region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
                                                                                                                                                                                                                 Talt351
/clone_lib="Triticum aestivum FGAS: TaLt3"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="genomic DNA"

strain="OTTH0595"

/db xref="reaxon:70448"

/clone="ota04c05.g"

/clone="ota04c05.g"

/clone="bb="Ostreococcus tauri genomic shotgun library"

/note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV;

Shotgun library prepared after monication of the genomic

DNA. Blunt ligation in EcoRV site of Bluescript. Size

selection of the inserts after agarose electrophoresis

between 1 and 3 Kb."
                                                             /db_xref="taxon:4565"
/lab_host="DH5 alpha"
                                                                                                       /mol_type="mRNA"
/cultivar="Wheat line CI 14106"
                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                 organism="Triticum aestivum"
                                                                                                                                                                                                               [124,739].
351 row: A column:
                                                                                                                                                                           . 872
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Pred. No. 0.0024;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Computer Science
57 Campus Drive, Saskatoon,
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Talt3 Triticum aestivum
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                                                                                                                                                                                                                                                                          Base calling software base calls. To aid in the software Lucy
                                                                                                                                                                                                                                                      sequence. Lucy identified
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                                                                                                                                           Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila NA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)
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BP 191 91006 EVRY cedex - FRANCE
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AL053013.1 GI:4934461
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BACR19D16 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCTCCAACTTGAGAAGTATCTTGGTGGT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
                                                                                                 organism="Drosophila melanogaster"
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Pred. No. 0.00
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survey sequence TET3 end of
rom Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (E-mail
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-mail : seqref@genoscope.cns.f)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqref@genoscope.cns.fr
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SOURCE

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Best Local :
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7
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Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola
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                                                                                                                                                                       This sequence is the direct result of the Base calling software phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aestivum cDNA,
DR741095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR741095 1133 bp
FGAS001026 Triticum aestivum FGAS:
                                                                                                                                                                                                                                                                                                                 Concordia University, Department of 7141 Sherbrooke St. West, Montreal,
                                                                                                                                                                                                                                                                                                                                                        Plant Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                          Contact: Patrick Gulick
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR741095.1 GI:70970528
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                                                                                                                                       the region [32,747]
Plate: L2B0204 rov
                                                                                                                                                                                                                                                      Email: pgulick@alcor.concordia.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSSBBSCTSTSSSSSSSYSSSTCSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACGAGACGCAGGCGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGSGYGKGCSSGSGBSCSCCSSCSCSCSCSCSCCSCSSCCSSSBSSSKCSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGCGCTGCCGATAAAGCTTGTCGAAGATGTCGGCTGCTTGCCGTTCGCCGCCGACGCG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSSDSTSTCCSCCCYMCTCCSTYBMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGSSSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGAGGGTCGACGAGAGGTCGTCGAGTTGCCCCGTAGTGCTTCAGCGTGTGGGCCGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTCGACCAGCTCGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGACTGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSASGSGSWSAGGGSGSTGSTSSSSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSSGSSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1133)
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514 848 2881
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/mol_type="mRNA"
/db xref="taxon:4565"
/db yref="Triticum aestivum FGAS: Library 2 Gate
/clone lib="Triticum aestivum FGAS: Library 2 Gate
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;
                                                                                                                   Location/Qualifiers
                                                                            organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924
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11.4%; Pred. No. 0.004;
                                                                                                                                       row: J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                       column:
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Library 2 Gate 3
                                                                                                                                                                                                                                                                                                                   Quebec
                                                                                                                                                                                                                                                                                                                                       Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                    Wheat and Canola Crops
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Triticum
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      Aerial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794
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RESULT 8
BI955767/c
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VERSION
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DEFINITION
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Best Local
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                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /1/ bp mRNA linear EST 19-OCT-200 HVSMEm0024G19f Hordeum vulgare green seedling EST library HVcDNA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA clone HVSMEm0024G19f, mRNA sequence.
B1955767
                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Total hq bases = 310
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 717)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGACCAGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGAGTCTAGGCGTGCCCCTGTCGTCAACGGGGATCCCCACCGTCTCCACCAGTCTGTT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGTAGCC-----GTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCCAGTGGCACAGAACGAGCAACGCAAGGGGCAACCTGCGATGAAACGCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTATGGCCAATACCTGCTCGACAATCTCGTGCCCCTTGAGGTTTCTCGCAAACCCTCC 527
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                                                                                                                                                                              quality sequence start: 4 quality sequence stop: 551. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 864 656 7288
864 656 4293
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/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEm0024G19f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parts (crown and leaf) of wheat cultivar Norstar from
                                                                           cultivar="Morex"
                                                                                                                              organism="Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:16302370
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58.1%;
                                                                                                        type="mRNA"
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Pred. No. 0.004;
0; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       SC 29634, USA
                                                                                                                                 subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1133;
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KEYWORDS

TITLE

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SOURCE

VERSION

FEATURES

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RESULT 9
CV948578/c
LOCUS
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                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
CV948578
CV948578.1
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1 (bäses 1 to 655)
Randal, T., Dwyer, R.A., Huitema, B., Beyer, K., Cvitanich, C., Randal, T., Dwyer, R.A., Gates, K., Roberts, S., Yatzkan, B., Gaffney, Kelkar, H., Fong, A.M., Gates, K., Roberts, S., Yatzkan, B., Gaffney, Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, Windass, J., Binder, A., Birch, P.R.J., Gisl, U., Govers, F., Gow, N.A Mauch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S., Lam, S.T. and Judelson, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CV948578 655 bp mRNA linear EST PVrpvb_12064 zoospores, purified Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora infestans (potato late blight agent)
Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCC-----GTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGACGCGCAGAACTGGCACGCGAAGGCCGCCTGAGACGAGACGCAGGCGCGTGT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTAGGCGTGCCCCTGTTGTCGACAGGGATCCCCACCGTCTCCACCAACCTGTTGTCCT 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGCTTGAGAAGTATCTTGGTGGT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XinoI; Morex (mla) plants were greenhouse grown in the R
Wise lab at lowa State University, Ames, IA; 7 day old
green seedlings were infected with isolate 5874 of
Blumeria graminis f. sp. hordei, and leaves were harvested
24, 48 and 72 hr post-inoculation and snap frozen (Wise).
In the TU Close lab at the University of California,
Riverside, total RNA was prepared from each sample pool,
equal quantities of all three RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plassmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Banbo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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HVcDNA0014 (Blumeria infected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IVCDNA0014 (Blumeria IIIIECTORI) | Site_1: EcoRI; Site_2: | | Note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: | | Note = | Note 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="green seedling leaf"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:58138334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%;
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Pred. No. 0.0044;
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                                                                                                     Gow, N.A.,
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AUTHORS
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CV948570/c
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PVrpvb_12056 :
sequence.
CV948570
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                                                                                                                                                                                                 l (bases 1 to 671)

1 (bases 1 to 671)

1 (bases 1 to 671)

Randall, T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C., Randall, T., Dwyer, R.A., Gates, K., Roberts, S., Yatzkan, E., Gaffney, T., Kelkar, H., Fong, A.M., Gates, K., Roberts, S., Yatzkan, E., Gaffney, T., Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, E., Windass, J., Binder, A., Birch, P.R.J., Gisi, U., Govers, F., Gow, N.A., Manch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S., Lam, S.T. and Judelson, H.S.

Large-scale gene discovery in the comycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora infestans (potato late blight agent)
Phytophthora infestans
Bukaryota; stramenopiles; Oomycetes; Pythiales; F
                      Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CV948570.1
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                                                                                                      Contact: Judelson HS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACTTTT
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                                                                                                                                                             Plant-Microbe Interact.
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/mol_type="mRNA"
/strain="88069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note="Vector: pSPORT1
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/sex="Al"
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Riverside,
4199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zoospores,
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Pred. No. 0.0055;
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                                                                                                                                                             18 (3),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pythiales; Pythiaceae;
                                                                                                                                                             229-243 (2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae;
Bukaryota; Viridiplantae; Streptophyta; Enbryophyta; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases; Tromesses; Hordeum.)
1 (bases; Tromesses; Namesses; Namesse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF265573 849 bp mRNA linear EST 23-OCT-2001
HY CEa0012L01f Hordeum vulgare seedling green leaf EST library
HYCDNA0004 (Blumeria challenged) Hordeum vulgare subsp. vulgare
CDNA Clone HY CEa0012L01f, mRNA sequence.
                                                                                                                                                                                   Email: LTALWEY 448
Total hg bases = 448
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        seedling leaf cDNA library 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mlai3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF265573.1 GI:11196567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF265573
                                                                                                                                                                                                                                                                                               Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                 Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                             quality sequence stop: !
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Phytophthora
/mol_type="mRNA"
/strain="88069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="zoospores,
/note="Vector: pSPORT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4787"
/sex="A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
/sub_species="vulgare"
/db_xref="taxon:112509"
                                                       cultivar="CI16155 (Mla13)"
                                                                                                   organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%;
55.7%;
                                                                             type="mRNA"
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Pred. No. 0.0055,
0; Mismatches (
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RESULT 12
CK152637/c
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Best Local Similarity
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Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilson, D.,
                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                      Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                       CK152637.1
                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CK152637 857 bp FGAS035711 Triticum aestivum FGAS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTTGAGAAGTATCTTGGTGGT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAGGCGTGCCCCTGTCGACAGGGATCCCTACCGTCTCCACCAACCTGTTGTCCTCC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGCACAAAACGAGCGACGCAAGGGGGCAGCCGACCTGTGATGAAACGCAGGCGGTGAGC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGCGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAGCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCCTTGAGGCCGTCGCGGCCC 90
                                                                                                    (bases 1 to 857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Whing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:39-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="TJC121"
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/tissue_type="seedling green leaf"
                                                                                                                                                                                                                                                                                                                                       GI:38971884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53.8; DB 2;
Pred. No. 0.0056;
0; Mismatches 72;
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TaLt3 Triticum aestivum
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                                                                                                                                                                                                 Tracheophyta;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 339)
Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
Anderson,O.A., Appels,R., Bailet,C., Gale,M., Graner,A.,
Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
                                                                                                                                                                                                                                                                                                       BB415712 339 bp mRNA linear EST 24-JUL-2000 MWL038.G04000426 ITEC MWL Wheat Root Library Triticum aestivum cDNA clone MWL038.G04, mRNA sequence.
                                                                                                                                                                                    Triticum aestivum
                                                                                                                                                                                                                                                            BE415712.1 GI:9413558
                                                                                                                                                                                                                                                                                    BE415712
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1C101 Engineering Building, 57
Saskatchewan, S7N 5A9, Canada
                                                                                                                                                                                                            Triticum aestivum (bread wheat)
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Plate: TaLt350 row: A column: 01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 306 966 1769
Fax: 306 966 2033
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Contact: Wm L Crosby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: fgas_ests@cs.usask.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGACCAGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGCCCGACGCGCAGAACTGGCACGCGAAGGGCGCACCCCGCCTGAGACGAGACGCAGGC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGTAGCC------GTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCCCAGTGGCACAGAACGAACGCAGCGAGGCGACCTGTGACGAAACACAGGC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTATGGCCAAGACCTGCTCGACAATCTCGTGCCCCTTAAGGTTCCTCGCGAACCCTCC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype CI14106 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H)(driver). Nitro-pyrole anchored oligo-dT priming and non-directional cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4565"
/lab_host="DH5 alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Wheat line CI 14106"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.4; DB 7;
Pred. No. 0.0071;
"" amatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Computer Science
57 Campus Drive, Saskatoon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stress In Wheat
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CD922535/c
                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                           KEYWORDS
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Best Local Similarity 58.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 GCCAGCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)

Contact: Warburton M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mwarburton@cgnet.com
International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Applied Biotechnology Center, CIMMYT
Apdo. Postal 6-641, 06600 Mexico DF |
Tel: 52-5-7269091 ext 1381
                                                                                                                                               Genoplante, a major partnership french program Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                 CD922535 528 bp
G750.103J05F010528 G750 Triticum
                                                      Genoplante
93, rue Henri Rochefor
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                          CD922535
CD922535.1
                                                                                                                                                                                                                                                                                  Triticum aestivum
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                Contact: Genoplante
                                                                                                                                                                                        Genoplante.
                                                                                                                                                                                                    Pooideae; Triticeae; Triticum.
1 (bases 1 to 528)
                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                     Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGCACAGAACGAGCAACGCAGGGGGCAGCCGACCTGTGACGAAACACAGGCGGTGAGC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGCGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCGAACAGGAACTTTGTCGT 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="root"
/dev stage="8 day old"
/clone_lib="ITEC MML Wheat Root Library"
/clone="Vector: pyES2 (Invitrogen); 0.5-1.5 Kbp average
insert size."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:4565"
clone="MWL038.G04"
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Pred. No. 0.0096;
0; Mismatches 7
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e G750103J05,
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RESULT 15
CK124607/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CK124607
BES1824109m05 I
MPMGp2010M059 S
                                                                                                                                                                            *Plant Protein Chip Group, Department Lehrach, **Department Molecular Genetics, Gene Expression Group *Max-Planck-Institute for Molecular Genetics, **Institute Genetics and Crop Plant Research Gaterslaben *Innestr. 73 , D-14195 Berlin, Germany, **Corrensstrasse Gaterslaben, Germany Gaterslaben, Germany Gaterslaben, Germany Gaterslaben, Germany **A+49(0)30/84131648, **+49(0)394825500 Fax: *+49(0)30/84131128, **+49(0)394825237 Email: *kersten@molgen.mpg.de, **weschke@ipk-gaterslaben.insert Length: 771 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                      Application of the protein microarray technology for the identification of expression library derived target proteins barley protein kinase CK2 Unpublished (2003)
Contact: Birgit Kersten* and Winfriede Weschke**
*Plant Protein Chip Group, Department Lehrach, **Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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CK124607.1 GI:44807609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kramer, A., Feilner, T., Possling, A., Radchuk, V., Weschke, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pooideae; Triticeae; Hordeum.
1 (bases 1 to 771)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGACCAGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTATGGCCAATACCTGCTCGACAATCTCGTGCCCCTTGAGGTTTCTCGCAAACCCTCC
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                                                                                                                                     primer: pQE65
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llarity 57.6%;
Conservative
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pollination)"
/clone_lib="G750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="recital"
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/cultivar="Barke"
/sub_species="vulgare"
/db_xref="GABI:945637"
                                                         /organism="Hordeum vulgare
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Triticum"
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                                                                                                                  ocation/Qualifiers
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BES1824 Hordeum vulgare subsp.
5-PRIME, mRNA sequence
                                                                                                                                                             column:
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Pred. No. 0.0098;
0; Mismatches 7
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Query Match 8.8%; Score 52.8; DB 7; Best Local Similarity 57.6%; Pred. No. 0.01; Matches 121; Conservative 0; Mismatches 77;
      233
                                                                                                                                                                                                                                                                                                                    144 GGTGTAGCC------GTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 CTCTATGGCCAACACCTGCTCGACTATCTCGTGGCCCTTAAGGTTCCTAGCAAACCCTCC 354
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                                                                GTCGACCAGCTCGAACAGGAACTTTGTCGT 221
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GTCCTCCAGCTTGAGAAGTATCTTGGTGGT 204
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/dev_stage="0-10 DAF (days after flowering)"
/lab_host="E. coli, SCS-1/pSE111"
/clone_lib="BES1824"
/clone_lib="Clones"
/clone_lib="Clones"
/clone_lib="Clones"
/clone_lib="Clones"
/clonestriction kit
/clonestriction kit
/clonestriction kit
/clonestriction site and a Sall adapter (Invitrogen). The main
/clonestriction site and a Sall adapter (Invitrogen). The main
/clonestriction site and a Sall adapter (Invitrogen). The main
/clonestriction site and a sall sate is NOT present, as well as the Sall Adapter
/clonestriction sites
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Search completed: April 7, 2006, 14:04:07 Job time: 2303.02 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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     Issued_Patents_NA:*

1: /cgm2_6/ptodata/1

2: /cgm2_6/ptodata/1

3: /cgm2_6/ptodata/1

4: /cgm2_6/ptodata/1

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-103-840A-1
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Sequence 3050, Ap
Sequence 6211, Ap
Sequence 6337, Ap
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Sequence 2148, Ap
Sequence 115, Ap
Sequence 1192, Ap
Sequence 1192, Ap
Sequence 1193, Ap
Sequence 112, Ap
Sequence 113, Ap
Sequence 113, Ap
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
9687, Ap	9729, Ap	<ol> <li>Appli</li> </ol>	7, Appli	15396, A	15284, A	2716, Ap	2972, Ap	15332, A	<ol> <li>Appli</li> </ol>	28, Appl	5616, Ap	5524, Ap	5676, Ap	5647, Ap	2990, Ap	2688, Ap	3181, Ap	13447, 7	13896, 7	13694, A

#### ALIGNMENTS

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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
ITITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 124; Conserv
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OTHER INFORMATION: "n" bases at various positions throughout the OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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Pred. No. 2e-09;
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RESULT 3
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US-09-902-540-9688, Application US/09902540
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APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sec
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/109/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10
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Matches 125
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Applic
Patent No. 6294328
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                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9688
LENGTH: 1080
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                       TYPE: DNA ORGANISM: Myxococcus xanthus
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                                         AGCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCCGGCCCGAC
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  AGTATCTGCCCCACGATTTCGCCGGGCGTCAGGTGGCGTGAGAGCCCCCATCTGCCCGGTG 372
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Pred. No. 4.2e-10;
0; Mismatches 79;
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                                                                                                                             Length 1080;
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APPLICANT: Slater, Steven C.
APPLICANT: Wisgand, Roger C.
APPLICANT: Wisgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1099
INVENTE: 13751
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                                                                                                                                                                                                                                                                       Sequence 3050, Application US/09902540 Patent No. 6833447
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Best Local Similarity
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APPLICANT: Hinkle, Gregory
APPLICANT: Slater, Steven C
APPLICANT: Wiegand, Roger C
                                                              APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                     PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10
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TYPE: DNA
ORGANISM: Myxococcus xanthus
NUMBER OF SEQ ID NOS: 16825
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Pred. No. 7e-10;
0; Mismatches 79;
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Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION MYXOCOCCUS Xanthus Genome Service Reference: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/99/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10
RESULT 7
US-09-252-991A-6211
; Sequence 6211, Application US/09252991A
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US-09-902-540-793
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; ORGANISM: Myxococcus xanthus
US-09-902-540-793
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.9
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 793
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LENGTH: 792
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Best Local Similarity
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ORGANISM: Myxococcus xanthus
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                                                                                                                         183 GAAATTGCCGTCGACCAGCTCGAACAGGAACTTTGTCGT 221
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                                                                                                                                                                                                                                                                                  CAGGIGICGCTIGAGGCCGTCGCGGCCCGACGCAGAACTGGCACGCGAAGGCGCACCC 122
                                                                                                                                                                                                                                                                                                                                                               CACGAGCCTGTTGACGCCGGGCCCGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGTAG 62
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 3; Ler Pred. No. 2.7e-09; 0; Mismatches 90;
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: REGUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PELICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6211
LENGTH: 456
TYPE: DAN
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6211
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; ORGANISM: Beeudomonas aeruginosa
US-09-252-991A-6337
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APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6337
LENGTH: 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6337, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                      Matches 108;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
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                                                                                  376
316
                                      156
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                                                                                                           96 GCAGAACTGGCACGCGAAGGCCGCCCGCCTGAGACGAAGACGCAGGCGGTGTAGCCGTC 155
                                                                                                                                                                                                       36 CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC
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GTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACTT
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                                                                                  GCAGAAACTGCAATCCAGGGCCAGCCCGCCTGGGAGGACACGCACAGGGTGCCGCGTCC
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                                                                                                                                                                                                                                                   Conservative
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Pred. No. 6.4e-07;
0; Mismatches 72;
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US-09-252-991A-6133
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6419, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6551795
GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         SEQ ID NO 6133
LENGTH: 1764
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Best Local :
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                           Similarity
GCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGTC 155
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                                                                   CACCTGGCCGATCACCTCGGCGGCGGTGAGGTCGCTGTTGAAACCCTGCTTGCCGGTGGA 1584
                                                                                                            CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC 95
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Pred. No. 6.8e-07;
0; Mismatches 72;
                                                                                                                                                                           Score 64.8; DB 3; Pred. No. 7.3e-07;
                                                                                                                                                         Mismatches
                                                                                                                                                       72;
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RESULT 11
US-09-605-703B-2129/c
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TYPE: DNA
ORGANISM: Corynebacterium glui
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1198)
OTHER INFORMATION: RXA01186
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PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 2129
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APPLICANT:
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BGI-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
                                                                                                          APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhar
APPLICANT: Schroder, Hartw
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gre
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CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
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PRIOR FILING DATE: 1999-07-08
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APPLICANT: Kroger, Burkhard
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Similarity 59.1%;
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                                                                                                                              Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
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Zelder, Oskar
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Pred. No. 2.4e-06;
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US-09-902-540-1116/c
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; LOCATION: (101)..(1198)
; OTHER INFORMATION: RXA01186
US-09-605-703B-2131
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SEQ ID NO 1116
; LENGTH: 15377
; TYPE: DNA
; ORGANISM: Myxococcus »
                                                                                                                                                                                                     Query Match
Best Local Sim
Matches 198;
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Best Local S
Matches 107
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PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 2131
LENGTH: 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1116, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome PILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEC.
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TYPE: DNA
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                                                                                                                                                                                                                      Local Similarity
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                                                                 11282 GAGGTTCCTTTTGAAGCCCAACTTCCCCGTCATGCAGAAGTCGCACGCCAGCGCACAGCC
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107; Conserv
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 CACCTGGCTGGAGACGCAGATGACGTACTTCTCATCGAAGATGGGGATGCGGACCGCTTC
                        CGCCTGAGACGAGACGCAGGCGGTGTA---GCCGTCGTGGCGACGGATCCGCACCGTCTC
                                                                                                  CAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGCGAGAACTGGCACGCGAAGGCGCACCC
                                                                                                                                CACCGGCCGGTCCCCTCCCCGGACCTGGAGCACCTGGTCCAATATCTCCCAGGTCTG
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Pred. No. 2.4e-06;
0; Mismatches 74;
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0; Mismatches
                                                                                                                                                                                                                   Score 61.4; DB
Pred. No. 8e-06;
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sec.
FILE REFERENCE: 38-10(15849)B
CUURRENT APPLICATION NUMBER: US/09/902,540
CUURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2548
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US-09-489-039A-4396/c
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Sequence 4396, Application US/0: Patent No. 6610836
GENERAL INFORMATION: APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC AVERTICAL OF INVENTION: PREUMONIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6833447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Myxococcus
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Pred. No. 6.5e-06;
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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96 8 US-10-611-442-2

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109 3 US-09-738-626-2214

100 3 US-09-738-626-214

101 3 US-09-738-626-1

102 3 US-09-74-300-6756

103 9 US-10-450-763-18200

104 10-450-763-12544

105 10-471-2045

105 10-154-163-1092

105 10-154-163-1092

105 10-151-740A-17

106 9 US-10-915-740A-17

107 107-108-1455-1468

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Sequence 2, Appli
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Sequence 25444, Ap
Sequence 2461, Ap
Sequence 2745, Ap
Sequence 2192, Ap
Sequence 17, Appl
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Sequence 1068, Ap
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10-156-761-4325	-10-156-761-2633	10-437-963-27652	US-10-425-115-173488	-10-425-115-88284	-10-437-963-40940	US-10-425-115-176166	US-10-425-115-142879	US-10-437-963-36501	<b>US-10-425-114-15465</b>	US-10-437-963-93881	Ľ	US-10-437-963-84904	ш	US-10-437-963-80449	US-10-329-624-1342	US-08-781-986A-1342	US-10-437-963-41296	16	US-10-487-901-2105	US-10-437-963-44594
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#### ALIGNMENTS

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APPLICANT: Hutchinson, C. Richard
APPLICANT: Katz, Leonard
APPLICANT: Reid, Ralph
APPLICANT: Reid, Ralph
APPLICANT: Hu, Zhihao
APPLICANT: Hu, Zhihao
APPLICANT: Gramajo, Hugo
ITITLE OF INVENTION: RECOMBINANT GENES FOR POLYKETIDE
ITITLE OF INVENTION: MODIFYING ENZYMES
FILE REFERENCE: 300622009100
CURRENT APPLICATION NUMBER: US/10/611,442
CURRENT APPLICATION NUMBER: US 60/393,016
PRIOR APPLICATION NUMBER: US 60/393,016
PRIOR APPLICATION NUMBER: US 60/393,016
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 17596
TYPE: DNA
ORGANISM: Micromonospora Megalomicea
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US-10-611-442-2
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                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 597; DB 8; Best Local Similarity 100.0%; Pred. No. 2.6e-167; Matches 597; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10611442 Publication No. US20040203015A1
                                                                                                                                                                                                                                                     17000 AACACGAGCCTGTTGACGCCGGGCCCGAGCGCCACCACCTGCTGCACGATCTCGCCGGGT 17059
                                                17120
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181 ATGAAATTGCCGTCGACCAGCTCGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGA 240
                                                                                                                                                                                    61 AGCAGGTGTCGCTTGAGGCCGTCGCGGCCCCGACGCGCAGAACTGGCACGCGAAGGCGCAC 120
                                                                                                                                                                                                                                                                                                   1 AACACGAGCCTGTTGACGCCGGGCCCGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGT
                                                CCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCG
                                                                                                                                                    AGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGCGCAGAACTGGCACGCGAAGGCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 17596;
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US-10-156-761-2608/c
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
APPLICANT: SHIBA, TADAYOSI
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2608
LENGTH: 1104
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2608, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                          Matches 124;
                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGAGTCTTTGCGCTGCCGATAAAGCTTGTCGAAGATGTCGGCTGCTTGCCGTTCGCCG 17359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCGCTCGGCGAGGGTCGACGAGAGGTCGAGTTGCCCCGTAGTGCTTCAGCGTGTGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTCGCCGAATGGGTAGACCCACGACCTGGGGGCGAAGCTGACATAGTCACCACCCTATCA 480
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                                AGACGCAGGCGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGT 193
                                                                                                      TGAGGCCGTCGCGGCCGACGCAGAACTGGCACGCGAAGGCGCACCCCCGGCCTGAGACG 133
                                                                                                                                                                       TGACGCCGGGCCCGAGCCAGCCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCT
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                                                                  CCAGGCCCGCCTGTCCGGTGGCGCAGAACGGGCAGTTCATACCGCACCCGGCCTGGGAGC 371
                                                                                                                                         TGAGCGCCCGCATGCCGTCCACGATCTGGTGCACGATCTCGCCGGTCGACAGGTTCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGTGCAAGAGACGTCAATTCGTCAAGTGACCACAGAGGAGCCTGACGATGGACGATGCT 17539
TGATGCACATCGTCACCCGGTCCGGGTAGCGCATGAGCACCGACTCGACGAGCGTCCCGT
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HORIKAWA, HIROSHI
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Pred. No. 9.5e-13;
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                                                                                                                                                                                                             78;
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; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; PEATURE:
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other
US-10-156-761-1
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Publication NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
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US-10-156-761-1
                                                                                                                                                                                                                                                                                                   US-10-470-565-1/c
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Best Local S
Matches 124
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Publication No. US20040126870A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin ver
SEQ ID NO 1
                                                             APPLICANT: Societe des Produits Nestle S.A.
TITLE OF INVENTION: NCC2705 - the genome of a
FILE REFERENCE: 80290/W0
CURRENT APPLICATION NUMBER: US/10/470,565
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: EP 01102050.0
PRIOR FILING DATE: 2001-01-30
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3221186 TGAGCGCCCGCATGCCGTCCACGATCTGGTGCACGATCTCGCCGGTCGACAGGTTCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                3221366
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                                                                                                                                                                                                                                                                                                                                                                                                                                           194 CGACCAGCTCGAACAGGAACTT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 TGACGCCGGGGCCCGAGCGCCAGCGACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 TGAGGCCGTCGCGGCCGACGCGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACGCAGGCGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGT
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                          version 3.1
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Pred. No. 2.2e-12;
0; Mismatches 78;
                                                                                                                                                                                             Bifidobacterium
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                                                                                                                                                                                                                                                                           ; ORGANISM: Corynebacterium glutamicum US-09-738-626-2214
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                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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Matches
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LENGTH: 1098
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                                                                                                                                                                                                                                      Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1885220 CGGCCACACGCACCTGTTCGATTATTTCACCGGTGGACATGTTACGGGTCAGGCCAAGCT 1885161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1885040
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                                                                                                                                                                                                                   Local Similarity
155 CGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                        406 CACAGAATGGGCACGCCATGCCGCAACCAGCCTGCGAAGAAATACACAGCGTGGÁGCGAT 347
                                                                                                                            466 GAACCTGATCCACGATCTCACCGATTGAAAGGTTACGGTCCAAACCGCCCTGACCAGTTG
                                                                                                                                                                                                    107;
                                                                                                                                                              35 GCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACG
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                                                                                        CGCAGAACTGGCACGCGAAGGCGCACCCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOKOI, HARUHIKO
TATBISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OZAKI, AKIO
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OCHIAI, KBIKO
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                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                Score 62.6; DB 3;
Pred. No. 2.1e-08;
0; Mismatches 74;
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Pred. No. 2e-11;
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION UNMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/25968
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SOFTWARE: PATENTIN VET. 3.0
TYPER: DNO 1
LENGTH: 3309400
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Sequence 6756, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity Matches 107; Conserv
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TATEISHI, NAOKO
SENOH, AKIHIRO
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HAYASHI, MIKIRO
OCHIAI, KEIKO
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OZAKI, AKIO
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Pred. No. 4.4e-08;
0; Mismatches 74;
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US-09-974-300-6756
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                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (403)..(1233)
; OTHER INFORMATION: 95% homologous to Escherichia coli similar to,accession
; OTHER INFORMATION: number D90881,Smith-Waterman Score=1342.
US-10-450-763-18200
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US-10-450-763-18200/c
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6756
                                                                                                                                              Query Match
Best Local S
Matches 96
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Publication No. US20050196754A1
GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 18200
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
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PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108;
                                                                       660 CACCTGGCCGATAATTTCCGACACCCGCAGGTTGCGGTTAAAGCCCCTGCTGGGCGGTGGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
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                           96 GCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGAGACGCAGGCGGTTAGCCGTC 155
                                                                                                            36 CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC
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 ACAGAATTTACACTCCAGCGCACACCCCACCTGCGAAGAGACGCAGAGCGTGGCACGGTC
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0; Mismatches
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                                                                                                                                            Score 56.4; DB 9;
Pred. No. 1.6e-06;
0; Mismatches 66;
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1.8e-07;
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US-10-450-763-25444/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2461, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
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SOFTWARE: Custom
SEQ ID NO 25444
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Best Local &
                NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASCSEQ for Windows Version
SEQ ID NO 2461
LENGTH: 594
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CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR PRIOR APPLICATION NUMBER: 09/540,217
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
                                                                                                        APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                        APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIMILAR LOCATION: (403)...(1233) LOCATION: (403)...(1233) OTHER INFORMATION: 95% homologous to Escherichia coli similar to,accession OTHER INFORMATION: number D90881,Smith-Waterman Score=1342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2493
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600 ACAGAATTTACACTCCAGCGCACACCCCACCTGCGAAGAGACGCAGAGCGTGGCACGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 GCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGAC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCTGGCCGATAATTTCCGACACCCGCAGGTTGCGGGTTAAAAGCCCTGCTGGGCGGTGGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCTTCCGGGATATACACCGTTTCGACGCGCTGATCGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56.4; DB 9;
Pred. No. 1.6e-06;
0; Mismatches 66;
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; LOCATION: 1...76; SEQUENCE DESCRIPTION: US-10-194-163-1092
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US-10-194-163-1092
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Query Match 9.0%;
Best Local Similarity 55.7%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1092, Application US/10194163
Publication No. US20020172976A1
GENERAL INFORMATION:
APPLICANT: Ross, Bruce Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 1092
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/194,163
FILING DATE: 04-Nov-2002
CLASSIFICATION: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Basu, Shantanu
REGISTRATION NUMBER: 43,318
REFERENCE/DOCKET NUMBER: 52928200010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                 FEATURE:
                                                                                                                                                              ANTI-SENSE: UNKNOWN ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYNUCLEOTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 TCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 cgcaccccgcctgagacgagacgcaggcggtgtagccgtcgtcgtggcgacggatccgcaccg 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426 CCGCTTTCATGTTCCGCTTTCAGCCGCCGAGGGTCAATGCTCATAAAGTACAGCCGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 CCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGCGCAGAACTGGCACGCGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCTCCCACCTGTGTCAGAACACAAACAGAATTGCCATATTCGTGCCGCATTAATACGG
                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 755 PAGI
                                                                                                               NAMB/KBY:
                                                                                                                                            ORGANISM: PORPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                        TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTCGATCGTGTAGCCGTCATGAAGCTCGAATAAAACTTCATTGT 261
                                                                                                                                                                                                                                                                       LENGTH: 7685 base pairs
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650-813-5995
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1...7685
                                                                                SEQ ID NO:
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Pred. No. 2.4e-06;
0; Mismatches 69;
 Score 53.8; DB 5;
Pred. No. 1e-05;
0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                   529282000101
                                                                                1092
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                               Length 7685;
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   Indels
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PILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UF 2001-272697
PRIOR APPLICATION NUMBER: UF 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2245
LENGTH: 2715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-156-761-2245
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US-10-156-761-2245/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2245, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2715
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                       1012
                                              772
                                                                                       248
                                                                                                                                   832
                                                                                                                                                                                                                           892
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                                                                                                                                                                                                                                                                                                                 952
308 CTTTGCGCTGCCGATAAAGCTTGTCGAAGATGTCGGCTGCTTGCCGTTCGCCGCCGACGC 367
                                                                                                                                                                           188 TGCCGTCGACCAGCTCGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGACTGCGCT 247
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                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                                                                                                                                                                                                                                                                                                                                8 GCCTGTTGACGCCGGGCCCGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGTAGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                     CGGCGAGGGTCGACGAGAGGTCGACGTTGCCCCGTAGTGCTTCAGCGTGTGGGCCGAGT 307
                                                                                                                                 ACTCGACGAACTTGCCGACGACGCCGTGCTTGCGCAGCATCTCGGTGATCGTGAGCACGA 773
                                                                                                                                                                                                                       ACATGTTGCCGATGGTGGCGCGGTTGGCGAGGCTCGTGGCCGCCACACCCTCGCCGTAGA
                                                                                                                                                                                                                                                                   GAGACGAGACGCAGGCGGTGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAAT 187
                                                                                                                                                                                                                                                                                                               GGTACTTCAGGGTCTCGTCGATCGGAAGATCGCGGCGGTGGAGCCGAACTCCGGCG 893
                                                                                                                                                                                                                                                                                                                                                        GTCGCTTGAGGCCGTCGCGGCCGACGCGCAGAACTGGCACGCGAAGGCGCACCCCGCCT 127
                                                                                                                                                                                                                                                                                                                                                                                                    GCTCCTTGGCGTACGCCTCGACGAGCGCGACCTGCTGCTCGTCACGGCCGGTCAGGCGCA 953
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                                           GGTCCGTGGCGGTCGTGCCGGGCTTGAGCTCACCGGTGAGCTTGAAGCCGACGACGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTCAGGGATAAGTACAGATTCCACGAAACGCCCTTCTCCTACGGGGAAGAGATACTTC
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 6;
Pred. No. 0.00013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2715;
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APPLICANT: Pizza, Mariagratia
APPLICANT: Grandi, Guido
ITITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
FILE REFERENCE: 002441.00090
CURRENT FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: US/10/915,740A
CURRENT FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR APPLICATION NUMBER: USSN 60/132,068
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US-10-915-740A-17
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US-10-915-740A-1068/c
US-10-915-740A-1068/c
; Sequence 1068, Application US/10915740A
; Publication No. US20050191316A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-915-740A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 60872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/10915740A Publication No. US20050191316A1
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APPLICANT: Hickey, Erin
APPLICANT: Peterson, Jeremy
APPLICANT: Tettelin, Herve
APPLICANT: Venter, J. Craig
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Local Similarity 54.3%;
                                                                                                                                                            8632 TCGAGT 8637
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Scarselli, Maria
Scarlato, Vincenzo
Rappuoli, Rino
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                                                                                                                                                                                                   TGTCGT 221
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                                                                                                                                                                                                                                                   CGATTCGGGGATGAAGACGGTTTCCACGCCGTTGCCCGTACCGACATCCAAAAGCCATTT
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Masignani, Vega
Galeotti, Cesira
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Tettelin, Herve
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Pred. No. 0.00017;
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Sequence 1455, Application US/10472928

| Publication No. US20050020813A1
| GENERAL INFORMATION:
| APPLICANT: CHIRON SpA
| APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
| TITLE OF INVENTION: STREPTOCCCCUS PNEUMONIAE PRO
| FILE REFERENCE: P026926WO
| CURRENT APPLICATION NUMBER: US/10/472,928
| CURRENT FILING DATE: 2003-09-26
| PRIOR APPLICATION NUMBER: GB-0107658.7
| PRIOR APPLICATION NUMBER: GB-0107658.7
| PRIOR FILLING DATE: 2001-03-27
| NUMBER OF SEQ ID NOS: 4979
| SOFTWARE: SeqWin99, version 1.03
| SEQ ID NO 1455
| LENGTH: 1083
| TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Grandi, Guido
TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
FILE REFERENCE: 002441.00990
CURRENT APPLICATION NUMBER: US/10/915,740A
CURRENT FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: 09/806,866
PRIOR FILING DATE: 1999-10-08
PRIOR PRILING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: USSN 60/103,794
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: USSN 60/132,068
PRIOR APPLICATION NUMBER: USSN 60/132,068
PRIOR PRILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-10-08
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US-10-472-928-1455/c
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; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-915-740A-1068
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Best Local Similarity 54.3%;
Matches 101; Conservative
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Scarselli, Maria
Scarlato, Vincenzo
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Masignani, Vega
Galeotti, Cesira
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Pred. No. 0.00024;
0; Mismatches 85
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Search completed: April 7, 2006, 04:35:58 Job time: 435.403 secs
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                                                                                                                                                                                                                                                          Query Match 8.2%; Score 48.8; DB 8; Length 1083; Best Local Similarity 53.7%; Pred. No. 0.00027; Matches 101; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
                                                                                                  242 AGATATTT 235
                                                                                                                                                   208 AGGAACTT 215
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Minimum DB
Maximum DB
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Perfect score:
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seq length: 2000000000
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1: geneseqn1980
2: geneseqn2000
3: geneseqn2001
4: geneseqn2001
6: geneseqn2002
7: geneseqn2002
8: geneseqn2002
9: geneseqn2003
10: geneseqn2000
11: geneseqn2000
11: geneseqn2000
12: geneseqn2000
14: geneseqn2000
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Listing first 45 summaries
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(c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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61.4	62.2	62.6	62.6	62.6	62.6	63.8	64.8	64.8	64.8	64.8	73.8	75	75	77.6	77.6	77.8	77.8	597	Score	
10.3 1537	10.4 2000	10.5 349980	10.5 349980	10.5 1098	10.5 1098	_	10.9 1764				12.4 349980	12.6 6713	.6	13.0 13751	13.0 1080	13.0 110000	13.0 110000	100.0 17596	Match Length	dp.
77 14	00 11	80 5	80 5	98 8	98 5	00 11	64 11	64 11	855 11	456 11	80 6	13 14	792 14	51 14	80 14	00	00 4	96 12	th DB	
ACL64653	ACL35412	AAH68530	AAH68531	ACA00654	AAH67179	ACL35016	ABD07529	ABD07815	ABD07733	ABD07607	ABQ81849	ACL64330	ACL66587	ACL64636	ACL73225	AAI99683_31	AAI99682_31	ADI14148	ID	
Acl64653 M. xanthu	Acl35412 Rice stre	Aah68530 C glutami	Aah68531 C glutami	Aca00654 C. glutam	Aah67179 C glutami	Acl35016 Rice stre		Abd07815 Pseudomon	Abd07733 Pseudomon	Abd07607 Pseudomon	Abq81849 Bifidobac	Acl64330 M. xanthu		Acl64636 M. xanthu	Acl73225 M. xanthu	Continuation (32 o	Continuation (32 o	Adil4148 M. megalo	Description	

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ALIGNMENTS	AEB66938 ADR08373	ADC75121 ADK52933	ADC76357 ADK54722	ADX46207 ADO84132	ADX10681	ABS56454_06	ABA57438 AAV52236	ADR93568	ABX06440 ADK43597	AAF21610	AAA81490 12	ACH98601	ABK75170	AAS82396	AAS89640		ABK79465	ACL66085
	Rice Pull	Rice F	DNA ho	Adx46207 Plant ful Ado84132 Plant ful	Adx64470 Plant ful Adx10681 Plant ful	ation (7	Aea57438 Streptoco Aav52236 Streptoco		Abx06440 S. pneumo Adk43597 Streptoco	Aaf21610 Neisseria	Continuation (13 o	Ach98601 Klebsiell			DNA		Baci	Acl66085 M. xanthu

ADI14148 standard; DNA; 17596 BP

ADI14148;

15-APR-2004 (first entry)

M. megalomicea cosmid KOS205-57-2.3B SEQ ID NO:2.

ds; polyketide; enzyme; MegR; MegR; MegK; MegCIV; MegBVI; MegBIII; MegL; MegM; megOsamine; megalomicin.

Micromonospora megalomicea.

WO2004003169-A2.

08-JAN-2004.

30-JUN-2003; 2003WO-US020681.

28-JUN-2002; 2002US-0393016P

(KOSA-) KOSAN BIOSCIENCES INC.

Hutchinson RC, Katz L, Reid R, H Z, Gramajo H;

WPI; 2004-203379/19.

Novel isolated, purified, or recombinant nucleic acid comprising polyketide modifying gene, there gene encodes polyketide modifying enzyme e.g., MegK, or MegM enzymes useful for producing modified polyketide.

Example 2; SEQ ID NO 2; 51pp; English.

ADII14148
ADII114148
ADII14148
AC ADII1
XX ILA
AC ADII1
AC ADII The invention relates to a novel isolated, purified, or recombinant nucleic acid (1) comprising a polyketide modifying gene, where the gene encodes a polyketide modifying enzyme chosen from MegR, MegF, MegK, MegCV, MegCV, MegBIII, MegL, and MegM enzymes. A method of the invention is useful for producing a modified polyketide, which involves culturing a recombinant cell comprising the recombinant nucleic acid

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RESULT 2
AA199682 31
Continuation (32 of 45
WP Sequence split into
WP Sequence split into
WP AA199682 01
WP AA199682 01
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WP AA199682 06
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Best Local
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 under conditions in which the cell expresses a product of a gene encoded by the nucleic acid under conditions in which the unmodified polyketide is present, and producing the modified polyketide. The cell produces megosamine and can attach megosamine to a polyketide, where the cell, it its naturally occurring non-recombinant state cannot produce megosamine. The present sequence contains downstream megalomicin modification enzyme genes.
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Pred. No. 1.4e-08;
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US AAI99683 Accession Aai99683
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                   10-JUL-2001; 2001US-00902540.
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                                                                                                                                                                                                                                                                                           Transgenic plant; DNA
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(MONS ) MONSANTO TECHNOLOGY LLC
                                              10-JUL-2000; 2000US-0217883P.
                                                                                            10-JUL-2001;
                                                                                                                                             21-DEC-2004
                                                                                                                                                                                           US6833447-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACL64636 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 9688; 25pp; English.
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Pred. No. 8.3e-09;
0; Mismatches 79;
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDs 1-1849 represent a set of 1849 contig and singleton sequences comprising coding sequences, DNA replication elements, promoters and other regulatory elements from the genome of the bacterium Myxococcus and other regulatory elements from the genome of the bacterium Myxococcus and thus. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
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                                                                                                                                                                                                          Myxococcus xanthus
                                                                                                                                                                                                                                                               Transgenic plant; DNA
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                                                                                                                                    21-DEC-2004.
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                                                        10-JUL-2000; 2000US-0217883P.
                                                                                             10-JUL-2001;
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                                                                                             2001US-00902540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
WPI; 2005-028716/03
                                                                                                                                                                                              Myxococcus xanthus.
                                                                                                                                                                                                                                                     M. xanthus DNA fragment, seq id 793
                                                                                                                                                                                                                                                                                 02-JUN-2005
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                                                                                                                                        21-DEC-2004.
                                                                                                                                                                    US6833447-B1
                                                                                                                                                                                                                          Transgenic plant;
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                                                     (MONS ) MONSANTO TECHNOLOGY LLC
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                          Hinkle GJ,
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                                                                                                                                                                                                                          replication; gene regulation; gene expression;
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340

280

400

62 0

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RESULT 8
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XX SYNTHE
XX SP1227
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Matches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SBQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SBQ IDs 1-1849 represent a set of 1849 contig and singleton sequences comprising coding sequences. DNA replication elements, promoters and other regulatory elements from the genome of the bacterium Mxyococcus xanthus. Note: The sequence data for this patent did not form part of the prince.
                                                                                                                                                                                                                                                                                                                                                                                                                                      identification;
rotavirus; food
                                                                                                                                                                                                                                                                                                                                                                                                                                                              antidiarrheic; antibacterial; inhibitor of Salmonella; detection;
identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
   WPI; 2002-668397/72
                                                                                                                  30-JAN-2001; 2001EP-00102050
                                                                                                                                                                           30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                                     31-JUL-2002.
                                                                                                                                                                                                                                                                                        EP1227152-A1
                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                         Bifidobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bifidobacterium longum NCC2705 related nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ81849 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ81849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6713 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing
                                                            (NEST ) SOC PROD NESTLE SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAATTGCCGTCGACCAGCTCGAACAGGAACTTTGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCTGAGACGAGACGCAGGCGGTGTAGCCGTCGTGGCGACCGATCCGCACCGTCTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGTTGCGCTTGAGCCCCATGGTGCCCGTCATGCAGAAGCCGCAGGCCATGGCGCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCGTTCTTGCGAACCTCGCGGTTCACCGCGTGGACCTGGGCCACAATCTCGCTGGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGAGCCTGTTGACGCCGGGCCCGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCTGCGTGGACACGCACAACGTCCTGCGGTCCTCGGTGGGCATGTAGACGGATTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGCGCCCGTCCCGCGTCTTCCACCGGTACTTGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                   composition; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 984 A; 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO 793; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%;
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Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 2234 G; 1263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                composition; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID:1105
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Query Match
Best Local Similarity
Matches 123; Conserv

Conservative

0;

Mismatches

12.4%;

Score 73.8; Pred. No. 1

.5e-07; DB 6; 82;

Length 349980 Indels

0,

Gaps

Sequence 349980 BP;

68046 A; 106490 C; 106389

<u>.</u>

69055 T; 0 U; 0 Other;

by the European Patent Office

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CC sequences given in ABQ81843 and ABQ81843, or a sequence spiven in ABQ81843 and ABQ81843, or a sequence spiven in CC ABQ81842 and ABQ81843, also described is a polynucleotide (II) encoding a CC fusion protein, comprising a sequence selected from 1097 sequences given in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a CC heterologous polypeptide. (I) has antidiarrheic and antibacterial CC activities, and can be used as an inhibitor of Salmonella. (I) (which is C a probe) is useful for the detection and/or identification of CC Bifidobacterium longum in a biological sample. A carrier containing the CC lactic acid bacterium gifidobacterium longum NCC2705 (CNCM I-2618) can be used for preventing and/or treating diarrhoea brought about by pathogenic CC used for preventing and/or treating diarrhoea brought about by pathogenic CC products, ice-creams, fermented cereal based products, milk based for preventing and/or treating diarrhoea brought about by pathogenic CC products, ice-creams, fermented cereal based products, milk based CC products, ince-creams, fermented cereal based products, milk based CC gowders, infant formula, pet food or a pharmaceutical composition CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the Expression of the Bifidobacterium gene. ARQ81844 to ARQ81850 represent CC insting from the present invention but not mentioned further within the sequence CC insting from the present invention but not mentioned further within the sequence of the printed specification but is based on sequence information or summited by the Enronean Datent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide comprising a probe or primer for detecting in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a pol sequence of a Bifidobacterium genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1105; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention describes a polynucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bifidobacterium genome sequence useful as and/or identifying Bifidobacterium longum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
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RESULT 9
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                                                                 antibacterial
                                                                               Bacterial infection; gene;
                                                                                                               Pseudomonas
                                                                                                                                                29-JUL-2004
                                                                                                                                                                                                                ABD07607
                                                                                                                                                                                                                                                                                                                                                                85096
                                                                                                                                                                                                                                                                                                                                                                                                                              85156 TGCCGGTGGCGCAGAACGGGCAGTCCATGCCGCAGCCGACCTGCGAGGAGATGCACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85216 CGGCCACACGCACCTGTTCGATTATTTCACCGGTGGACATGTTACGGGTCAGGCCAAGCT 85157
                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCCGACGCGAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGAGACGCAGGCGG
                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                              ACAGGAACTITGICGICTGGCTICC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCCGTCGC
                                                                                                                                                                                                                                                                                                                                                                TGGTGCGGGTCGCGTATCGCATAAGCACCGATTCGATGAGGGAGCCGTCGAACAGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                              TGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGA 205
                                                                                                                                                                                                                                                                                               ACAAGGTCTTGATGGTGCCTTC 85012
                                                                                                              aeruginosa polynucleotide #6211
                                                                                                                                              (first entry)
                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                456
                                                                                ds;
                                                                                                                                                                                                                ВP
                                                                                Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                               85037
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US6551795-B1

Pseudomonas aeruginosa

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RESULT 10
ABD07733/c
ID ABD077
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as ta components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other seq of Pseudomonas species using biochip technology. Sequences ABD01397 ABD17967 represent P. aeruginosa polynucleotides of the invention. The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-615309/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a pathological infection, for evaluating a compound, such as a polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-2003
                          Pseudomonas aeruginosa
                                                                  Bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial drugs,
US6551795-B1
                                                       antibacterial.
                                                                                               Pseudomonas
                                                                                                                           29-JUL-2004
                                                                                                                                                     ABD07733;
                                                                                                                                                                                 ABD07733 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to Pseudomonas aeruginosa polypeptides and the
                                                                                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                 156
                                                                                                                                                                                                                                                                                                              204
                                                                                                                                                                                                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                          108;
                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                             GCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
                                                                                                                                                                                                                                                     GCAGAAACTGCAATCCAGGGCGCAGCCCGCCTGGGAGGACACGCACAGGGTGCCGCGTCC
                                                                                                                                                                                                                                                                                                                                                                 CACCTGGCCGATCACCTCGGCGGCGGTGAGGTCGCTGTTGAAACCCTGCTTGCCGGTGGA 203
                                                                                                                                                                                                                                                                                 GTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACTT
                                                                                                                                                                                                                                                                                                                                                                                           CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6211; 455pp; English
                                                                                             aeruginosa polynucleotide #6337.
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP;
                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0074788P
98US-0094190P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 A; 142 C; 147
                                                                                                                                                                               DNA;
                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%;
                                                                  gene;
                                                                                                                                                                                  855
                                                                    ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deloughery C,
                                                                                                                                                                                  ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64.8; DI
Pred. No. 8.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                    Pseudomonas
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                                                                    aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                    infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    456;
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ABD07815/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999;
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                            Pseudomonas aeruginosa
                                                             antibacterial.
                                                                             Bacterial
                                                                                                           Pseudomonas
                                                                                                                                          29-JUL-2004
                                                                                                                                                                        ABD07815;
                                                                                                                                                                                                      ABD07815 standard; DNA; 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                                                                                    376
                                                                                                                                                                                                                                                                                     316
                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                 436 CACCTGGCCGATCACCTCGGCGGCGGTGAGGTCGCTGTTGAAACCCCTGCTTGCCGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108;
                                                                                                                                                                                                                                                                                                                                                                         96 GCAGAACTGGCACGCGAAGGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGTC
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                                                                                                                                                                                                                                                                                     855
                                                                                                                                                                                                                                                                                                                   GTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACTT
                                                                                                                                                                                                                                                                                                                                                    GCAGAAACTGCAATCCAGGGCGCAGCCCGCCTGGGAGGACACGCACAGGGTGCCGCGTCC
                                                                           infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6337; 455pp;
                                                                                                         aeruginosa polynucleotide #6419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                         (first
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98US-0094190P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 A; 270 C; 263 G;
                                                                                                                                         entry)
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                                                                           gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64.8; DB 11;
Pred. No. 9.1e-06;
0; Mismatches 72;
                                                                                                                                                                                                         쁌
                                                                           Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
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155 377 95

317

US6551795-B1

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RESULT 12
ABD07529
ID ABD07529
ID ABD07529
XX ABD07
XX ABD07
XX PBew
XX Bact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therefore therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial dargs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa capacet components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences of feeducemonas species using biochip technology. Sequence ABD11397-CABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                     Bacterial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                     Pseudomonas
                                                                                                                                                        29-JUL-2004
                                                                                                                                                                                                                        ABD07529 standard; DNA; 1764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 6419; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1998;
27-JUL-1998;
     US6551795-B1
                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                           GTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCTGGCCGATCACCTCGGCGGCGGTGAAGGTCGCTGTTGAAAACCCTGCTTGCCGGTGGA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGC 95
                                                                                                                                                                                                                                                                                                             GCAGAAACTGCAATCCAGGGCGCAGCCCGCCTGGGAGGACACGCACAGGGTGCCGCGTCC
                                                                                                                   aeruginosa polynucleotide #6133
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                                                                                                                                                     (first entry)
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98US-0094190P.
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                                                                                     gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64.8; DB 11;
Pred. No. 9.5e-06;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP
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                                                                                                                                                                                                                          ВP
                                                                                   Pseudomonas aeruginosa infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a CC prophylaxis and treatment of pathological conditions resulting from a CC deterial infection, for evaluating a compound, such as a polypeptide, CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa-derived peptides or polypeptides, as target CC components for diagnosis and/or treatment of P. aeruginosa-caused CC infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                     ss; abiotic agriculture.
                                                            Oryza sativa
                                                                                                                                                                                                             Rice stress-regulated promoter
                                                                                                                                                                                                                                                                             02-JUN-2005
                                                                                                                                                                                                                                                                                                                                      ACL35016;
                                                                                                                                                                                                                                                                                                                                                                                                  ACL35016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1764 BP; 308 A; 544 C; 557 G; 355 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful as molecular targets for diagnostics, prophylaxis and treatment pathological conditions resulting from bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-2003.
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                                                                                                                                                       stress
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                                                                                                                                                                                                                                                                         (first entry)
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98US-0094190P
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                                                                                                                                                       tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                  CDNA;
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0; Mismatches
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Pred. No. 16
                                                                                                                                                       transgenic plant; plant; cereal;
                                                                                                                                                                                                                    SEQ ID NO:13579
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72;
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95

WO2003008540-A2

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RESULT 14
ARH67179/C
ID ARH67
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AC ARH67
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AC ARH67
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DT 26-SE
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DE C 911
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KW COLYT
KW Organ
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24-AUG-2001;
26-SEP-2001;
21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kreps J,
Moughamer
                                                                                                                                 7179/C
AAH67179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responsiveness of a plant, e.g. cereal stress, salt stress or osmotic stress.
Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                         26-SEP-2001
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                                          glutamicum coding sequence fragment SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                ACGAGACGCAGGCGGTGTAGCCGTCGTCGCGACGGATCCGCACCGTCTCGATGAAATTGC
                                                                                                                                                                                                                                                                                                                          GGTTGAAGCCCTGGGTGGCGGTGGAGCAGAACGTGCAGTTCAGGCCGCAACCGACCTGCG
                                                                                                                                                                                                           TGCCATCCACGCCCATCGCCAGCAGCCACTTGTGGGTGCCGTCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                      TGCCCAGGTGGCGTGCGGCAACCCCACACCTGGCCGATGATCTCGGCGGTGGTCAGGTTGC
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T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2001US-0300112P.
; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
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                                                                         (first entry)
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                                                                                                                                 DNA; 1098
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N, Ricke
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Pred. No. 1.8e-
0; Mismatches
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D, Zhu T;
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RESULT 15
ACA00654/c
ID ACA00654 standard; DNA; 1098 BI
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AC ACA00654;
XX
DT 03-JUN-2003 (first entry)
XX
DE C. glutamicum derived ORF SEQ:
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07-APR-2000;
03-AUG-2000;
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Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2000; 2000EP-00127688
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                                                                                                                                                                                                                                                                                                          CACAGAATGGGCACGCCATGCCGCAACCAGCCTGCGAAGAAATACACAGCGTGGAGCGAT
                                                                                                                                                                                                                                                                                                                                     CGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGT
                                                                                                                                                                                                                                                                                                                                                                      GAACCTGATCCACGATCTCACCGATTGAAAGGTTACGGTCCAAACCGCCCTGACCAGTTG
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Senoh A,
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2000JP-00159162.
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Ikeda
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da M,
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Pred. No. 3.1e-05;
0; Mismatches 74
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Ozaki A;
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glutamicum derived ORF SEQ

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Search completed: April Job time: 343.371 secs
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Best Local S
Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1098 BP; 221 A; 295 C; 304 G; 278 T; 0 U; 0 Other;
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                                                                                                                                                                                                          CGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAACT 214
                                                                                                                                                                                                                                                                         CACAGAATGGGCACGCCATGCCGCAACCAGCCTGCGAAGAAATACACAGCGTGGAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                              GCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGCGGCCCGACG 94
                                                                                                                                                                                                                                                                                                                       CGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGGTGTAGCCGT 154
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                   7,
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                     2006, 03:16:51
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Pred. No. 3.1e-05;
0; Mismatches 74; Indels
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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GenEmbl:*
1: gb ba:*
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597
1 aacacgagcctgttgacgcc.....cacgaacgcgcagcgggggc 597
                                                                                                                                                                                                                                                                                                                                                                                                                                             5883141 seqs, 28421725653 residues
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		P			SUMMARIES	
Result No.	Score	Query	Query Match Length	BB	ID	Description
C 1	87.4	14.6	110000	-	BA000043 11	Continuation (12 o
N	87	14.6	301332	_	AE017237	AE017237 Mycobacte
u	84.4	14.1	110000	_	BA000045 22	Continuation (23 o
C 4	83.2	13.9	308050	_	SC0939124	AL939124 Streptomy
c 5	81.2	13.6	207050	_	AL646063	AL646063 Ralstonia
6	78.4	13.1	110000	_	AP006618_42	Continuation (43 o
7	77.8	13.0	110000	_	AE000516_31	Continuation (32 o
ი 8	77.8	13.0	110000	_	AE017333 17	Continuation (18 o
ი 9	77.8	13.0	110000	Н	CP000002_17	Continuation (18 o
10	77.8	13.0	318050	ш	BX248344	BX248344 Mycobacte
11	77.8	13.0	348676	ب	BX842581	BX842581 Mycobacte
c 12	77.6	13.0	1080	6	AR628287	AR628287 Sequence
c 13	77.6	13.0	13751	6	AR619704	AR619704 Sequence
14	77.2	12.9	110000	_	BA000030_32	Continuation (33 o
c 15	76	12.7	10719	_	AE001946	AE001946 Deinococc
c 16	75	12.6	792	0	AR621649	AR621649 Sequence
17	75	12.6	6713	σ	AR619398	AR619398 Sequence
c 18	75	12.6	110000	_	BX571965 17	Continuation (18 o

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45	44	43	42	41	40	39		37	36			33		31			28	27	26	25				21	20	19
62.6	62.6	62.6	63.2	63.6	64.2	64.8	64.8	65	65	65.6	65.8	66.2	67	68	69.6	72	72.2	72.6	73.4	73.4	73.8	73.8	73.8	74.6	74.6	74.6
10.5 110000	10.5 1098	10.5 1098	10.6 348408	10.7 49742	10.8 349652	10.9 17148	10.9 1993	10.9 110000	10.9 110000	11.0 110000	11.0 110000	11.1 110000	11.2 110000	11.4 300217	11.7 110000	12.1 110000	12.1 110000	12.2 110000	12.3 110000	12.3 110000	12.4 349980	12.4 349980	12.4 110000	12.5 348934	12.5 348642	12.5 347894
1 BA000036_21	6 AX122298	6 BD164415	1 BX248358	1 AP008226 18	1 BX569690	1 AE004798	1 PSEPILF	1 CP000089_32	1 CR931997 13	1 AE017180_11	1 AP008231_24	1 CR555306_07	1 AP006840_14	1 AE016922	1 AE017282_30	1 CP000088 07	1 BA000035_20	1 CP000090_22	1 CP000010_14	1 CP000010 13	6 AX553954	6 AX492787	1 AE014295_04	1 BX640417	1 BX640446	1 BX640431
Continuation (22 o	AX122298 Sequence	BD164415 Novel pol	BX248358 Corynebac	Continuation (19 o	BX569690 Synechoco	AE004798 Pseudomon	L49434 Pseudomonas	•	Continuation (14 o		•		Continuation (15 o	AE016922 Chromobac	Continuation (31 o	0			Continuation (15 o	Continuation (14 o	AX553954 Sequence	AX492787 Sequence	Continuation (5 of	BX640417 Bordetell	BX640446 Bordetell	BX640431 Bordetell

## ALIGNMENTS

36 fragments LOCUS BA000043 Accession Begin End 1 10000 100001 310000 300001 410000 400001 510000 600001 710000 600001 1010000 1000001 1110000 1100001 1210000 1100001 1310000 1100001 1510000 1100001 1510000 1100001 1510000 1200001 1510000 1300001 1510000 1300001 1510000 1300001 1510000 1500001 1510000 1500001 2010000 1600001 2010000 1600001 2710000 2800001 2810000 2800001 2810000 2800001 2810000 2800001 2810000 2800001 2710000 2800001 3310000 3000001 3310000 3300001 3310000 3300001 3310000 3300001 35544776	BA000043_35	یاں	1 1	BA000043_31	BA000043_30		BA000043_28	BA000043_27	BA000043_26	BA000043_25	BA000043_24	BA000043_23	BA000043_22		BA000043_20	BA000043 19	BA000043_18	BA000043_17	BA000043_16			BA000043_13		BA000043 11		- 1	- 1		- 1		- 1			1		ent Nam	Sequence split into	WACCOMMENT TI/C	,
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Mycobacterium avium subsp. paratuberculosis str. k10
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2.9e-05;
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'transI_table=11
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complement (6994. .7788)
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7961. .8734
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       Fragment Name BA000045 01 BA000045 03 BA000045 06 BA000045 06 BA000045 11 BA000045 12 BA000045 12 BA000045 12 BA000045 12 BA000045 12 BA000045 13 BA000045 22 BA000045 23 BA000045 33 BA000045 34 BA00
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CCCGCCACAACGTCTTTCGGGTCTGGC 246176
                                                   GCTCGAACAGGAACTTTGTCGTCTGGC 226
                                                                                                         ACACCGTGTTGCGGTGCGGGTAGCGCATCAGCACCGACTCCACGGTGACCCCATCCAGGG 246149
                                                                                                                                              AGGCGGTGTAGCCGTCGTGGCGACCGATCCGCACCGTCTCGATGAAATTGCCGTCGACCA 199
                                                                                                                                                                                                                  CGCCCTGGCCGGTCGCGCAGAACGGGCAGGCCATGCCGCCTGCGACGAGATGC 246089
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SCO939124/c
                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                        Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H., Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M. Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S. Huang, C.H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neil, S., Rabbinowitsch, E., Rajandream, M.A., Rutherford, K., Rutter, S., Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S., Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrell, B.G., Parkhill, J., and Hopwood, D.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308050 bp DNA linear BCT 16-APR.
Streptomyces coelicolor A3(2) complete genome; segment 21/29.
AL939124 AL023797 AL031031 AL031035 AL031124 AL031225 AL031231
AL031260 AL034447 AL035559 AL035569 AL355913 AL645882
AL9399124.1 GI:24413886
                                                                        Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: sdb@sanger.ac.uk
On or before Oct 26, 2002 this sequence version replaced
gi:20520664, gi:20520751, gi:20520752, gi:20520665, gi:20520811,
gi:20520756, gi:20520845, gi:20520760, gi:20520817, gi:20520818,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria, Actinobacteria, Actinobacteria, Actinobacteria, Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                            coelicolor A3(2)
Nature 417 (6885), 141-147
                                                                                                                                                                                                                  Bentley, S.D.
                                                                                                                                                                                                                                                                                                                      Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTTGCGGGCAAAACCGGATTGGCCGGTGGCGCAGAAGCGGCAGGCCATGGGACAACC 31301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCCGGCGGCCGAAACCCTTCCTGCACCGTGAGCACCTGATCGACGATCTCGTGCACACC 31241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATTGCCGTCGACCAGCTCGAACAGGAACTTTGTCGTCTGGCTTCCCCTGGTGCGACT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCTGCGACGAAACGCAGACCGTCAGCCGCTCGGCGGCCGGAATACCCACGGTCTCGAC 31361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCTGAGACGAGACGCAGGCGGTGTAGCCGTCGTGGCGACCGGATCCGCACCGTCTCGAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGTGTCGCTTGAGGCCGTCGCGGCCCGACGCGCAGAACTGGCACGCGAAGGCGCACCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACGAGCCTGTTGACGCCGGGCCCGAGCGCAGCACCTGCTGCACGATCTCGCCCGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCACGACCTGCG 31435
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                                                                                                                                                                                                                                         (bases 1 to 308050)
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4200001 4310000
4300001 4410000
4400001 4510000
4500001 4650019
4600001 4659019
7) of BA000045 from k
                1. .308050
organism="Streptomyces coelicolor A3(2)"
                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    base 2200001 (BA000045 Gloeobacter violaceus
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Howarth, S.,
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                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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SC8D9.08"

gene="SCO5496"

possible hydrophobic

codon\_start=1/ transl\_table=11

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membrane

regions"

/product="putative small membrane hydrophobic protein" /protein id="CAB37572.1" /db\_xref="GI:4467247"

1672.

/note="TTA Leu codon, /gene="SC05495"

possible target for

bldA regulation"

note="Pfam match to /gene="SC05495"

entry PF00990 DUF9, 70, E-value 3.9e-46"

Domain

œ,

score

/note="Pfam match function 2, score

to entry PF00563 DUF2, Domain of unknown 291.30, E-value 1.2e-83"

/gene="SC05495"

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with the first 300aa Containing several potential membrane spanning hydrophobic regions and the remainder of the protein showing similarity to the phosphodiesterase mentioned above. Also similar to a nearby gene on the same cosmid (SCBD9.22) fasta scores; opt: 736, z-score: 625.6, E(): 5.3e-30, (33.6% identity in 729 as overlap). Contains TTA Leu codon, possible target for bldA regulation. Also contains Pfam match to entry PF00990 DUF9, Domain of unknown function, score 166.70, E-value 3.9e-46 and Pfam match to entry PF00563 DUF2, Domain of unknown function, score 16.70 and though function 2, score 291.30, E-value 1.2e-83. Contains possible hydrophobic membrane spanning regions"
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LVVAEGVEDDETWERLRDLGCDAVQGWLVAAAMPPEETTAWLLARGSRGWVRAAAALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC05495"
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SGS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="UniProt/TrEMBL:Q9Z583"
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
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JOURNAL
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 AGACGCAGGCGGTGTAGCCGTCGTGGCGACGGATCGCACCGTCTCGATGAAATTGCCGT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                            Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA
                                                                                                                                                                                                                                                                                                                                            Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.
URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ralstonia solanacearum
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ralstonia solanacearum GMI1000
segment 7/19.
AL646063 AL646052
AL646063.1 GI:17428161
                                                                                                                                                                                                                                                                                                Genome sequence of Nature 415 (6871),
                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                    2 (bases 1 to 207050)
Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raistonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL646063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGACCAGCTCGAACAGGAACTTTGTCGT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATGCACATGGTCACCCGGTCCGGGTAGCGCATGAGCACCGACTCGACGAGCGTCCCGT 162329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGGCCGTCGCGGCCGACGCGCAGAACTGGCACGCGAAGGCGCACCCCGCCTGAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCGCCCGCATGCCGTCCACGATCTGGTGCACGATCTCGGCGGTCGACAGGTTGCGGT 162449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACGCCGGGCCCGAGCGCCAGCACCTGCTGCACGATCTCGCCCGGTAGCAGGTGTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAACAGCTTCCACAGCGTCTTGCGCGT 162301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTVLDAALLHEVIAGHDPMDSTŠIDAPVBAVVBAARNGSVDGMRVGVVKQFRGEGYQA
GVVQRFDESVELLKSLGABIVELDCSSFDLALSAYVLIAPSECSSNLARFDGLRYGAR
VGDDGTHSABEVTSLITERAGFGFBVKRRIMLGTYALSGSYDDAYYGSAQKVRTLIKQS
FERAFEQVDVIVSFTTPTTAFAIGERADDPMAMYLADLCTIPTNLAGNAAMSLFCGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contains possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEDNLPVGLQIIAPAMKDDRLYKVGAAVEAAFVEKWGHPLIEEAPSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative membrane
/protein_id="CAB37576.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="SC8D9.12, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCO5500"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="GI:4467251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%;
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                                                                                                                                                                                                                                                                                                     the plant pathogen Ralstonia solanacearum 497-502 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83.2; DB 1;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207050 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Demange, N.,
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COMMENT
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/db_xref="Unitprot/TrrmhL:Q87096"
/db_xref="Unitprot/TrrmhL:Q87096"
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/translation="whelplyaargvQpGLAGGRPAQLLGGLSPRDPWRTHWQKXPL
/translation="whelplyakgrrapdvssrliaqdrygrmproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperproperp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene name confidence: probable predicted by Codon usage predicted by Homology predicted by FrameD"
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complement(332..1561)
/gene="RSC1148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="RROBABLE PKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (ROTAMASE) PROTEIN"
/protein_id="CAD14851.1"
/db_xref="G1:17428163"
/db_xref="GCA:Q8Y095"
/db_xref="InterPro:IPR001179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="CONSERVED HYPOTHETICAL PROTEIN"
/protein id="CAD14850.1"
/db_xref="GI:17428162"
/db_xref="InterPro:IPR003347"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (332. .1561)
/gene="RSc1148"
/note="Product confidence: probable
Gene name confidence: hypothetical
predicted by Codon usage
predicted by FrameD"
                                                                                                                                                                                                                                                           complement (2152. .3216)
/gene="RSC1150"
/note="synonym: RS04601"
complement (2152. .3216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="InterPro:IPR001179"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="slyD"
/note="synonyms: RS04602, RSc1149"
1573. .2097
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/transl_table=11
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/transl_table=11
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note="Product confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VADEDDEEPPRTLH"
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/note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="GMI1000"
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                                                                                                                                                                    /gene="RSc1150"
/function="miscellaneous; unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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// protesti_id="ROBIABLE SI."

// db_xref="ROBIABLE SI."

// db_xref="ROBIABLE SI."

// db_xref="ROBIABLE SI."

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// db_xref="InterPro:IPR007659"

// db_xref="InterPro:IPR007659"

// db_xref="InterPro:IPR007650"

// db_xref="InterPro:IPR
                                                                                                                                                           Gene name confidence : probable predicted by Codon usage predicted by Homology predicted by FrameD"
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predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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synthesis, modification; dna - replication, repair
restr./modif."
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LFHIRARRLASDIAPSTPQQ"
                                                                                                                                                                                                                                                                                                                                           complement (5960. .6853)

/gene="RSC:152"
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/function="Product confidence : probable
/note="Product confidence : probable
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/evidence=not_experimental
/trans1 table=11
/product="PROBABLE DNA MISMATCH REPAIR PROTEIN"
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/gene="RSC1152"
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IDPDSMTPRDĀLDALYRLKALSDASA"
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/evidence=not_experimental
/trans1 table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonym: RS04599"
protein_id="CAD14854.1"
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RESULT 6
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/note="synonym: RS04598"
6966. .8168
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/function="cell processes; transport of
/function="cell processes; transport of
/note="Product confidence: putative
Gene name confidence: hypothetical
predicted by Codon usage
predicted by Homology
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Pred. No. 0.00027;
0; Mismatches 83
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Pred. No. 0.00088;
0; Mismatches 101;
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nilarity 61.7%;
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Pred. No. 0.0011;
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Best Local Similarity 63.8
Matches 118; Conservative
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Pred. No. 0.0011;
D; Mismatches 67;
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RESULT 10
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Best Local :
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                                                                                                                     complete genome.
Mycobacterium bovis AF2122/97
Mycobacterium bovis AF2122/97
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
  Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe
Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.
Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., G
                                                           Garnier, T., Biglmeier, K., Camus, J.-C., Medina, N., Mansoor, H.
                                                                                                                                                                                                                              BX248344 BX248333
BX248344.1 GI:31
                                                                                                                                                                                                                                                                      Mycobacterium bovis subsp. bovis AF2122/97
                                                                                                        tuberculosis complex.
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Pred. No. 0.0011;
0; Mismatches 67;
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                                      Monsempe, C., Simon, S.,
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JOURNAL
REFERENCE
AUTHORS
TITLE
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Direct Submission

Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire

Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire

Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex

15, France. e-mail:tgarnier@pasteur.fr Submitted on behalf of the

Mycobacterium bovis sequencing teams, TB Research Group, Veterinary

Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone,

Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus,

Hinxton, Cambridge CB10 1SA, UK. Pr4 Annotation, Genopole, Institut

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Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28

rue du Docteur Roux, 75724 Paris Cedex 15, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The complete Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hewinson, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len: 258 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 258 aa overlap). Probable short-chain dehydrogenase/reductase (EC 1...-.) highly similar to various dehydrogenases e.g. O88068 |SCI35.33c PROBABLE DEHYDROGENASE (SDR PAMILY) from Streptomyces coelicolor (260 aa), PASTA scores: opt: 1208, E(): 2e-68, (72.35% identity in 253 aa overlap); Q9I376 |PAL649 from Pseudomonas aeruginosa PROBABLE SHORT-CHAIN DEHYDROGENASE (253 aa), PASTA scores: opt: 569, E(): 2.1e-28, (39.2% identity in 255 aa overlap); Q9EX74 |MLHA SDR-LIKE ENZYME from Rhodococcus erythropolis (246 aa), PASTA scores: opt: 567, E(): 2.8e-28, (41.15% identity in 248 aa overlap); etc. Also similar to many Mycobacterium tuberculosis dehydrogenases e.g. PABG3 |Rv2002 |MT2058 |MTCY39.16c PUTATIVE OXIDOREDUCTASE (260 aa), PASTA score: (38.3% identity in 248 aa overlap). BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY."
                 /note="Mb2883c, aldC, len: 455 aa. Equivalent to Rv2858c, len: 455 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 455 aa overlap). Probable aldC, aldehyde dehydrogenase (EC 1.2.1.3), similar to many e.g. O88069|SCI35.34c PUTATIVE ALDEHYDE DEHYDROGENASE from
                                                                                                                                                                                                                                                              /translation="mmdlsqrlagrvavitgggsgiglaagrrmragativvgdvdv
Eaggaaadelsglfvetdvcdeda/nglfdgaaetygridiafnagisfpednilen
Telaamqrvqdvnlksvylccraalrhmvlagkgsivnafsvavmgsatsqisytas
KGGVLamsrelgvqearqgirvnalcegfvntpllqelfakvferaarrmvhvflgrp
AEPDEIAAAVAFLASDDASFITASTFLVDGGISSAYVTPL"
Streptomyces coelicolor (483 aa), FASTA scores: opt: 1872
                                                                                                                                                                                 /locus_tag="Mb2883c"
complement(872. .2239)
                                                                                                                                                                                                                                                                                                                                                                /db_xref="GOA:Q7TXP6"
/db_xref="InterPro:IPR002198"
/db_xref="InterPro:IPR002347"
/db_xref="UniProt/TrEMBL:Q7TXP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
/product="PROBABLE SHORT-CHAIN TYPE
/product="PROBABLE SHORT-CHAIN TYPE
DEHYDROGENASE/REDUCTASE"
/protein_id="CAD96569.1"
/protein_id="CAD96569.1"
/db_xref="G1.31619629"
                                                                                                                                                                                                                                            complement (872. .2239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (99. .875)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="Mb2882c"
                                                                                                                     /locus_tag="Mb2883c"
/BC_number="1.2.1.3"
                                                                                                                                                                                                                       'gene="aldC"
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/note="Mb2882c, -, 1
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                                                                                                                                                                gene="aldC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                len: 258 aa. Equivalent to Rv2857c,
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E(): 6.4e-109, (64.5% identity in 448 aa overlap);
OSFABI ALDH BT-ALDH ALDEHYDE DEMYDROENASE from Bacillus
thermoleovorans (497 aa), FASTA scores: opt: 1157, E():
2.1e-64, (44.3% identity in 458 aa overlap); 033455 CYMC
p-CUMIC ALDEHYDE DEHYDROGENASE from Pseudomonas putida
(494 aa), FASTA scores: opt: 1149, E(): 6.5e-64, (43.15%
identity in 452 aa overlap);
identity in 452 aa overlap);
p40047 DHA5 YEAST | ALD5 | ALDH5 | ALD3 | YERO73W ALDEHYDE

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DESTINACIONASE IMASINALDS | ALD3 | YERO73W ALDEHYDE DESTINACIONASE from Saccharomyces cerevistae (Baker's yeast) (519 aa), FASTA scores: opt: 1091, E(): 2.7e-60, (38.55% identity in 459 aa overlap);
P80668 | FRAB ECOLI | PADA | MAOB | B1385 PHENYLACETALDEHYDE DEHYDROGENASE (EC 1.2.1.39) from Escherichia coli strain K12 (499 aa), FASTA scores: opt: 1074, E(): 3e-59, (42.3% identity in 462 aa overlap); etc. Also similar to many M. tuberculosis dehydrogenases e.g. P71823 | RV0768 | MTC7369.13 (489 aa), FASTA score: (38.1% identity in 467 aa overlap). Contains PS00687 Aldehyde dehydrogenases glutamic acid active site and PS00070 Aldehyde dehydrogenases cysteine active site. BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY."
                                                                                                                                                                                                                                                                                                                                                                                                                                        /motes "MDJ2884C, ", len: 308 aa. Equivalent to Rv2859c, /notes "MDJ2884C, ", len: 308 aa, Equivalent to Rv2859c, len: 308 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 308 aa overlap). Possible amidotransferase (EC 6.3.5. - or 2.-.-), equivalent (but longer 58 aa) to Q9CBU9|ML1573 POSSIBLE AMIDOTRANSFERASE from Mycobacterium leprae (249 aa), FASTA scores: opt: 1226, E(): 3e-64, (71.55% identity in 239 aa overlap). Also similar to other amidotransferases and hypothetical proteins, but shorter in N-terminus e.g. 088072|SCI35.37 PHYPOTHETICAL 25.3 KDA PROTEIN from Streptomyces coelicolor (242 aa), FASTA scores: opt: 683, E(): 1.2e-32, (47.65% identity in 235 aa overlap); AAK79730|Q97188|CAC1764 PREDICTED GLUTAMINE AMIDOTRANSFERASE from Clostridium acetobutylicum (241 aa), FASTA scores: opt: 458, E(): 1.6e-19, (32.95% identity in 246 aa overlap); AAK75201|Q97QV9|Sp1089 GLUTAMINE AMIDOTRANSFERASE CLASS I from Streptococcus pneumoniae (229 aa), FASTA scores: opt: 431, E(): 5.6e-18, (34.75% identity in 236 aa overlap); etc. Contains three 17 aa repeats at the N-terminus very similar to those in other Mycobacterium tuberculosis proteins e.g. Q1669|YY30 MYCTU|Rv2090|MT2151|MTCY49.30
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GFWFPPTVLTPKRGDRTVTDE I FGPVVVVLTFDDEADAI SLANDTAYGLSGS I WTDDL
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Best Local Similarity 61.7%;
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Mycobacterium tuberculosis H37Rv
Mycobacterium tuberculosis H37Rv
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium, Mycobacterium
                                                                                                                                                      complete genome.
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Pred. No. 0.00092;
0; Mismatches 77;
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Re-annotation of the genome sequence of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of M. tuberculosis sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology (Reading,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 348676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/M_tuberculosis/).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(374. .409)
/note="36 bp direct repeat, 36 out of 36 bp id
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (148. .4539)
/note="4392 bp direct repeat region"
complement (148. .183)
/note="36 bp direct repeat, 36 out of 36 bp identical to
sequence GTCGTCAGACCCAAAACCCCGAGAGGGGACAGC"
                                                                         /note="36 bp direct repeat, 36 out of 36 bp identical
sequence GTCGTCAGACCCAAAACCCCGAGAGGGGACGGAAAC"
                                                                                                                                                                                       /note="36 bp direct repeat, 36 out of 36 bp identical to
sequence GTCGTCAGACCCAAAACCCCGAGAGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                       /note="36 bp direct repeat, 36 out of 36 bp id
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="36 bp direct repeat, 36 out of 36 bp id
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="36 bp direct repeat, 35 out of 36 bp identical
sequence GTCGTCAGACCCAAAACCCCGAGAGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="36 bp direct repeat, 35 out of 36 bp identical
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="36 bp direct repeat, 35 out of 36 bp identical to
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGACGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                     complement (590. .625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (519. .554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:83332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L. .348676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mycobacterium tuberculosis H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lement (447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engl.) 148 (PT 10), 2967-2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .482)
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   repeat,
   36 out
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   of 36 bp identical
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                                                                                                                                                                                                                                                                                                                                                                  complement (2464. .2790)
/locus tag="Rv2815c"
complement (2464. .2790)
/locus tag="Rv2815c"
/function="REQUIRED FOR T
                                                                                                                                    /note="Rv2815c, (MTCY16B7.28), len: 108 aa. Probable transposase, identical from as 51 with P19772|YIA2 MYCTU PUTATIVE TRANSPOSASE (INSERTION ELEMENT IS986) from Mycobacterium tuberculosis (59 aa), FASTA scores: opt: 365, E(): 1.1e-19, (96.6% identity in 59 aa overlap); and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /t-anblation="iltrpladhqqqhegpdolrwgvesictqutelgvpiapstyyd
/tranblation="iltrpladhqqqhegpdolrwgvesictqutelqmtk
Hinrepsreelrogelkehisgvhaanygvygarkyweltlineegievarctverlmtk
LGLSGTTRGKARRTTIADPATARPADLVQRREPPAPARKHWADLTYVSTWAGFAYVA
FVTDAYARRIIGWRVASTWALDAIEQALWTRQDEGVLDLKOVIHHTDRGSQYTS
IRFSERLAEAGIQPSYGAVGSSYDNALAETINGLYKTELIKPGKPWRSIEDVELATAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Rv2814c, (MTCY16B7.29), len: 312 aa. Probable transposase, highly similar to others e.g. p97137|Rv0796|MTV042.06 PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS986/IS6110 from Mycobacterium tuberculosis (328 aa), FASTA scores: opt: 2103, E(): 6.1e-132, (100.0% identity in 312 aa overlap); etc. Start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1396. 1431)
/note="36 bp direct repeat, 36 out of 36 bp id
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGGAGGGAAAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WVDWFNHRRLYQYCGDVPPVBLEAAYYAQRQRPAAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="PROBABLE TRANSPOSASE"
/protein_id="CAB03675.1"
/db_xref="GI:3261653"
/db_xref="GOA:P19774"
/db_xref="UnlProt/Swiss-Prot:P19774"
/db_xref="UnlProt/Swiss-Prot:P19774"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1529. .>2467)
/locus_tag="Rv2814c"
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sequence GTCGTCAGACCCAAAACCCCGAGAGGGGACGGAAAC"
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complement(1248. .1283)
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sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGACGGAAAC"
complement(1176. .1211)
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/note="36 bp direct repeat, 36 out of 36 bp identical sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGAACGGAAAC"
complement (958. .993)
                                                                                                                                                                                                                                                                                                                                   ELEMENT IS6110."
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/locus_tag="Rv2814c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGACGGAAAC*
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product="PROBABLE TRANSPOSASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="20 bp partial direct repeat, CCCCGAGAGGGGGAGACGGAAAC,
of sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGGACAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insertion_seq="IS6110-11"
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                                                                                                                                                                                                                                                                                                                                                                          THE TRANSPOSITION OF THE INSERTION
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Best Local &
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                                             Sequence 9688
AR628287
   Unknown
                             AR628287.1
                                                                           AR628287
                                                                                                                                                                                                                                                                                                      GECCCGACGCGCAGAACTGGCCACGCGAAGGCGCACCCCGCCTGAGACGAGACGCAGGCGG
                                                                                                                                                                                                                                                                                                                                                                CGAGCGCCAGCACCTGCCACGATCTCGCCCGGTAGCAGGTGTCGCTTGAGGCCGTCGC
                                                                                                                                                                                  ACAGGAACTTTGTCGTCTGGC 226
                                                                                                                                                                                                                                         TGTAGCCGTCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGA
                                                                                                                                                                                                                                                                         GGCCAGTGGCACAGAACGGCAAGCCATGCCGCAGCCGGCCTGCGAGGAAATGCAGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="36 bp direct repeat, 36 out of 36 bp identical
sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGACGGAAAC"
complement(2976..3011)
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/db_xref="G1:164906"
/db_xref="G2:164906"
/db_xref="COA:050686"
/db_xref="InterPro:IPR002514"
/db_xref="InterPro:IPR002514"
/db_xref="IniProt5w18s-Prot:Q50686"
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sequence GTCGTCAGACCCCAAAACCCCGAGAGGGGAACGGAAAC"
complement(3049 .3084)
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/note="36 bp direct repeat, 36 out of 36 bp identical
sequence GTCGTCAGACCCCAAACCCCGAGAGGGGACGGAAAC"
complement (3624. .3659)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="36 bp direct repeat, 36 out of 36 bp identical
sequence GTCGTCAGACCCCAAAACCCCCGAGAGGGGACGGAAAC"
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125; Conserv
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Goldman, B.S., Hinkle, G.J., Slater, S.C. and Wiegand, R.C.
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Goldman, B.S., Hinkle, G.J., Slater, S.C. and Wiegand,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTATOTGCCCCACGATTTCGCCGGGCGTCAGGTGGCGTGAGAGCCCCCATCTGCCCGGTG 372
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                                   TCGTGGCGACGGATCCGCACCGTCTCGATGAAATTGCCGTCGACCAGCTCGAACAGGAAC
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/mol_type="genomic
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AE001946 AE001
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                                        white, O., Bisen, J.A., Heidelberg, J.P., Hickey, B.K., Peterson, J.D., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Moffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M., Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Fraser, C.M. et al. Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 Science 286 (5444), 1571-1577 (1999)
2 (bases 1 to 10719) White,O., Eisen,J.A.,
                                                                                                                                                                                                            Deinococcus radiodurans
                                                                                                                                                                                                                                                          AE001946.1
                               10567266
                                                                                                                                                                Deinococcaceae; Deinococcus.
1 (bases 1 to 10719)
                                                                                                                                                                                             Bacteria; Deinococcus-Thermus;
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 Heidelberg, J.F.,
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Pred. No. 0.0014;
0; Mismatches 78;
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 Hickey, E.K.,
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FEATURES
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Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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1109. .3043
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rloddlsermttwrtlpapeseagpeedaaaadagedon"
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SHVNLIPMPNDGSDFVSSSEEQIQAFYDALQDRGVDVSVRRSRGKDAGAACGQLALR
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drelsaaaaxvltgtdratillrqsbblltaqnnlrgalnaassarqebrrlpaaiire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DR0936"
4977. .6017
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identified by sequence
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Search completed: April Job time: 2893.48 secs
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Best Local S
Matches 124
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                                                                                        5205 TGAGGGTGAACAGATATTTGACCG 5182
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124; Conservative
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                                                                                                                                  CCAGCTCGAACAGGAACTTTGTCG 220
                                                                                                                                                                                      CGCAGATGGTCTTGCGGTCGAGGTAAGGCATGTACACCGCTTCCATCTGCCGCCCGTCGT 5206
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AEHAQAAQALVAAGYGGILNFAPVVLQTQDLHLPEAFAAPGRREVTVENVDFLAGMK
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ARAELYPPRGQTLRNPAPAAAAEAPATPEPASEPAPTPAETPTAAPAPAGPVYVQVGA
FUNVEGAQRFVEQLRAQGFSPSVNAPETGKVTVLLGPLTGSDLTSTEGRLDAAGLDHF
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              7,
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                   2006, 16:57:46
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:*
2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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length: 2000000000
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       gcctcctacgcggcgcaa.....ggaccgcctcaccgcgcact
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       6210
6360
10524
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110970
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(c) 1993 - 2006 Biocceleration
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   14 US-11-143-980-1
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14 US-11-056-470-2
14 US-11-075-185-37
14 US-11-075-185-3
14 US-11-175-689-3
14 US-11-175-689-3
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18 US-11-075-185-3
19 US-11-254-686-11
19 US-11-254-686-11
19 US-11-251-284-658
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10613.880 Million cell updates/sec
Sequence 1, Appli
Sequence 2, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 3, Appli
Sequence 34, Appli
Sequence 35, Appli
Sequence 27, Appli
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Sequence 37, Appli
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## ALIGNMENTS

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APPLICANT: Hocul, John
APPLICANT: Haltli, Bradley A.
APPLICANT: Haltli, Bradley A.
APPLICANT: Wagenar, Melissa M.
APPLICANT: Graziani, Edmund
APPLICANT: Summers, Mia
APPLICANT: Summers, Mia
APPLICANT: Summers, Mia
APPLICANT: Pong, Kevin
TITLE OF INVENTION: Biosynthetic Gene Cluster for
TITLE OF INVENTION: Polyketide
FILE REFERENCE: AM-101426US
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US/11/143,980
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: US 60/664,483
PRIOR FILLNG DATE: 2005-03-23
PRIOR PILLNG DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LEWITH: 116656
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US-11-143-980-1
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                                                                                                                                                                       Matches 349;
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                        LENGTH: 116856
TYPE: DNA
ORGANISM: Streptomyces sp.
                                                                                                                                                                                             Local
  52660
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                                                                                                                                                                                         h 29.1%;
Similarity 57.7%;
GECCTGGTGGCCACCTCCATCGCCTGGGGGGCTGTGGGCCGGTGACGGCATGGGCGAGGGC 52719
                                        egecreccegreaccrearcecrregeercregeeccegecagaacaregeccegrace
                                                                                   GGCAACTACGCACCCGGCCATGTCTTCGTGGACACGCTGGCCGAGCAGCAGCGGCCGAG
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                                                                                                                                                                       Conservative
                                                                                                                                                                    Pred. No. 1.5e-29;
0; Mismatches 229;
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US-11-056-470-1
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                                     US-11-056-470-1
                                                                                                                                                                PRIOR APPLICATION NUMBER: US 10/212,962
PRIOR FILLING DATE: 2002-08-05
PRIOR PELLORITION NUMBER: US 60/310,779
PRIOR FILLING DATE: 2001-08-06
PRIOR FILLING DATE: 2001-08-06
PRIOR FILLING DATE: 2002-06-14
PRIOR PELLORITION NUMBER: US 60/393,929
PRIOR PELLORITION NUMBER: US 60/393,929
PRIOR PELLORITION NUMBER: US 60/393,929
PRIOR APPLICATION NUMBER: US 60/395,275
PRIOR PELLORITION NUMBER: US 60/395,275
PRIOR FILLING DATE: 2002-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/11056470 Publication No. US20050261263A1
                                                                                                               SOFTWARE: FastSEQ
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SANTI
APPLICANT: MYLE
APPLICANT: TIAN
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BENZOQUINONE ANSAMYCINS FILE REPERENCE: 300622007510 CURRENT APPLICATION NUMBER: US/11/056,470 CURRENT FILING DATE: 2005-02-11
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                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                      ORGANISM: Streptomyces
                                                                          TYPE: DNA
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MYLES, David C.
TIAN, Zong-Qiang
HUTCHINSON, C. Richard
JOHNSON, Robert G., Jr.
ZHOU, Yi-Qing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGCCCGGCTGGTCCGAGCCGAGGTGGCAGCGTGCTGGGCCACGGCACGGTG
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 Score 150.4;
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Matches 332; Conservative
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                                                                                     GCGGTGACCGGGGTGGCCACGACCATCGTCTTCGACCACCCGACAGTGGACCGC
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CTCACCGAGC
                                 CTCACCGCGC 598
                                                                GCGGCGACCGGGCTGCGGCTCCCCGCCACGTTGCTCTTCGACCACCCGACTCCGGCTCTT
                                                                                                                                                                 GCCTTCCGTGACCTGGGATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCG
                                                                                                                                                                                                                                 CGAGCCGAGGTGGCAGCGGTGCTGGGCCACGGCACGCCGACGGTGATCGAGCGTGACGTC
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US-11-056-470-2
US-11-056-470-2

| Sequence 2, Application US/11056470
| Publication No. US20050261263A1
| GENERAL INFORMATION:
| APPLICANT: SANTI, Daniel V.
| APPLICANT: MYLES, David C.
| APPLICANT: HTIAN, Zong-Qiang
| APPLICANT: HOTCHINSON, C. Richard
| APPLICANT: JOHNSON, Robert G., Jr.
| APPLICANT: JOHNSON, Robert G., Jr.
| APPLICANT: FENG, Li
| TITLE OF INVENTION: BENZOQUINONE ANSAMYCINS
| TITLE REFERENCE: 300622007510
| CURRENT APPLICATION NUMBER: US/11/056,470
| CURRENT FILING DATE: 2002-08-05
| PRIOR APPLICATION NUMBER: US 60/310,779
| PRIOR APPLICATION NUMBER: US 60/310,779
| PRIOR APPLICATION NUMBER: US 60/389,255
| PRIOR FILING DATE: 2002-06-14
| PRIOR FILING DATE: 2002-06-14
| PRIOR FILING DATE: 2002-07-03
| PRIOR APPLICATION NUMBER: US 60/393,929
| PRIOR APPLICATION NUMBER: US 60/395,275
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RESULT 4
US-11-075-185-37
; Sequence 37, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
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TYPE: DNA
; ORGANISM: Streptomyces geldanus
US-11-056-470-2
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Best Local Sin
Matches 327;
  SEQ ID
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SEQ ID NO 2
                                                       FILE REPERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                     APPLICANT: REEVES, CHRISTOPHER
APPLICANT: JULIEN, BRYAN
APPLICANT: REID, RALPH
NUMBER OF SEQ ID NOS: 61
SOPTWARE: PatentIn version 3.3
EQ ID NO 37
                                                                                                                                                                                                    TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2002-07-12 NUMBER OF SEQ ID NOS: 10
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FastSEQ for Windows
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Pred. No. 4.6e-20;
0; Mismatches 250
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; TYPE: DNA
; ORGANISM: Sorangium
US-11-075-185-1
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                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.3 SEQ ID NO 1
                                                                                                                                                                                                                                                                    Matches 172;
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/11075185 Publication No. US20050266434A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR PRIOR PRIOR ON THE PRIOR PRIOR PRIOR PRIOR DATE: 2004-05-04
PRIOR PILING DATE: 2004-05-04
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GGCTCGACTCCCTCACCGCGGTCGAGCTGCGGAACCGGCTGGCGGCGCGCGGAACGCAA
                               GATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCGGCGGTGACCGGGGTCC
                                                                                                 CGGTGCTGGGCCACGGCACGGTGATCGAGCGTGACGTCGCCTTCCGTGACCTGG 484
                                                                                                                                  GACGGCCCCAGAGCGAACGATTCGCGGCGGTCCTCGAGCTCGTCAGGGCGGAGGCGGCGC 37064
                                                                                                                                                              CGATGCCGGAGCCCGACCGAGCATGTCGCCCGGCTGGTCCGAGCCGAGGTGGCAG 424
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                                                                  GCGTGCTCCGGCTGCCGGGGGCCGCCAGTGCCGCCAGATCGGCCGCTCAAGGAGCTGG
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REID, RALPH
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Pred. No. 1.4e-13;
0; Mismatches 118;
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RESULT 6
US-11-175-689-3
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SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.2%;
Best Local Similarity 49.0%;
Matches 301; Conservative
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APPLICANT: LEADLAY, PETER F.

APPLICANT: SWALL, PAMELA L.C.

APPLICANT: JOHNSON, PAUL D.R.

APPLICANT: JENKIN, GRANT A.

APPLICANT: DAVIES, JOHN K.

APPLICANT: HAYDOCK, STEPHEN F.

APPLICANT: HAYDOCK, STEPHEN F.

APPLICANT: HAYDOCK, STEPHEN F.

APPLICANT: NOVEL POLYKETIDES, THERAPEUTIC AND PROPHYLACTIC USES

FILE REFERENCE: 03495.0329-01
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APPLICANT: COLE, STEWART T.
APPLICANT: LEADLAY, PETER F.
APPLICANT: SWALL, PAMELA L.C.
APPLICANT: JOHNSON, PAUL D.R
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CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: 10/987,592
PRIOR FILING DATE: 2004-11-15
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TYPE: DNA
ORGANISM: Mycobacterium ulcerans
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 GTCGCCTTCCGTGACCTGGGATTCGACTCCATGACCGGCCGTCGACCTGCGGAACCGGCTC
                                                                                                                              GCGTCGA-----TGCCGGAGGCCGAACGTCACGAGCATGTCGCCCGGCTG
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                                                                                               CTGACGAGCAAATTAGCCGGACTAACGGCGACAGAACAGCGTGCAGTCACCCGGAAGTTG
                                                                GTCCGAGCCGAGGTGGCAGCGGTGCTGGGCCACGGCACGCCGACGGTGATCGAGCGTGAC
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Pred. No. 1.1e-12;
0; Mismatches 298;
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US-11-075-185-34
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   CGGAACCGGCTCGCGGCGGGTGACCGGGGTCCGGGTGGCCACGACCATCGTCTTCGACCAC
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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-34
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TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR
FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
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SOFTWARE: PatentIn versi
SEQ ID NO 34
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Best Local Similarity
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GTGCCCGCGGACAAGCCGCTGAAGGAGCTGGGGCTCGATTCGCTCACGGCCGTCGAGCTG
                                        ATCGAGCGTGACGTCGCCTTCCGTGACCTGGGATTCGACTCCATGACCGGCGTCGACCTG 513
                                                                                       TIGOTOGAGOTIGOGOGOGAGGTGGOGGTGGTGGTGGGGGAGGTCCGGGGAG
                                                                                                                                    GICGCCCGGCTGGICCGAGCCGAGGTGGCAGCGTGCTGGGCCACGGCACGCCGACGGTG
                                                                                                                                                                              CAGGAATCGGATCTCGCCCGGCGGCGGCTGGCGTCGATGCCGGAGGCCGAACGTCACGAGCAT 393
                                                                                                                                                                                                                                                                                                                  CTGTCGGCGCTCCAGCGTGCGGCGAGCGACGCCGGACGGGTGCCGCCGCTGCTGCGCGGG
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No. US20050266434A1
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49.7%;
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Pred. No. 2.4e-12;
0; Mismatches 273;
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APPLICANT: STINEAR, TIMOTHY P.

APPLICANT: COLE, STEWART T.

APPLICANT: LEADLAY, PETER P.

APPLICANT: SMALL, PAMELA L.C.

APPLICANT: SMALL, PAMELA L.C.

APPLICANT: JOHNSON, PAUL D.R.

APPLICANT: JOHNSON, PAUL D.R.

APPLICANT: DAVIES, JOHN K.

APPLICANT: HAYDOCK, STEPHEN F.

COTITLE OF INVENTION: THE MYCOLACTONE LOCUS: AN ASSEMBLY LINE FOR PRODUCING TITLE OF INVENTION: OVEL POLYKETIDES, THERAPEUTIC AND PROPHYLACTIC USES FILE REFERENCE: 03495.0329-01

CURRENT FILING DATE: 2045-07-07

PRIOR APPLICATION NUMBER: US/11/175,689

CURRENT FILING DATE: 2005-07-07

PRIOR APPLICATION NUMBER: 10/987,592

PRIOR APPLICATION NUMBER: 10/510.664
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US-11-175-689-1
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SEQ ID NO 1
LENGTH: 50973
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/519,864
PRIOR FILING DATE: 2003-11-14
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  GTCCTTGATCAAGCCGCATCCGTTCTCGGGTACGCCTCAACTGAGAGTCTCGATACTCAT 33393
                                     CTGACGAGCAAATTAGCCGGACTAACGGCGACAGAACAGCGTGCAGTCACCCGGAAGTTG
                                                                                                                                                             ACAGAGGTAATGGCTTACCGCGAGTCGATGCGCTCAAGCTCTGCATCGACGGCGACGCTC 33273
                                                                                                                                                                                                   GGTGGGGTCCGCGCGGGGCCGAGGAGACCGGTCAGGAATCCGGATCTCGCCCGGCGGCTG 360
                                                                                                                                                                                                                                             TGGGATCGGTTCTACCCCACATTCGCTTTGGCGCGACCGAGGCCCTTCCTACACGAAATC
                                                                                                                                                                                                                                                                                 GAGGAGCTGCGGACCACCCTGGACGCCGGGGGACCCCGTGGGTGTCGGTGGACCTGGAC
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48.9%;
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                                                                                                                   TGCCGGAGGCCGAACGTCACGAGCATGTCGCCCGGCTG 405
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FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
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US-11-075-185-35
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Matches 315; Conservative
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SEQ ID NO 35
LENGTH: 10968
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APPLICANT: REEVES, CHRISTO
APPLICANT: JULIEN, BRYAN
APPLICANT: REID, RALPH
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5140 GCGGGCGCGCTGCTCGAGCTGGTGCGCGCGCGGCGGCGGCCGTGCTGCAGCTGGCAGGT 5199
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                                     CACGAGCATGTCGCCCGGCTGGTCCGAGCCGAGGTGGCAGCGGTGCTGGGCCCACGGCACG
                                                                                                                                                                                                                                                                                                                       GGGCTGCCGGTCACCTCGATCGCCTGGGGTCTGTG-----GGCCGGGCAGAACATGGCC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGTGCCGGCGATGAGCCTCGCCTGGGGCTTCTGGGGAGCAGGCCGGGCTCGGCATGACG 4839
                                                                             GCCGCGACCGGAGCGGCGCGCTGCGCGCGCGCTCTCGGCGCTGCCCGAGGCCGAGCGG
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Pred. No. 2.9e-11;
0; Mismatches 263;
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RESULT 10
US-10-522-037-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 37507
TYPE: DNA
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Best Local
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CURRENT APPLICATION NUMBER: US/10/522,037
CURRENT FILING DATE: 2005-01-24
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Method for the TITLE OF INVENTION: cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                          13690
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TTCCGTGACCTGGGATTCGACTCCATGACCGCGTCGACCTGCGGAACCGGCTCGCGGCG
                                            CGCGAGGTGGGCGAGATCCTG---CGCATCCCGCCGGACCGCCTCGATACGCGCCAGCCC
                                                                                                                                                      GAGCTGGGCGCGCGCGACGACGCGAAGGACGACGACCGCCGCGCGCGAGCTGCGC
                                                                                                                                                                                                                                                                                         CGGGCGATCGAGGAGCTGCGGACCACCCTGGACGCCGGGGACCCCGTGGGTGTCGGTGGTG
                                                                                                                                                                                                                                                                                                                  CACGAGAAGGTGAAGCCCTGCAGACGCACATGGGCGCCACCGCACTCGAGTCGGAG
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                                                                  CGCCTCGCCAACGAGCTGGACGCCTCCGAGCTCTCGGCGATGTTCACCGACCTGCTGCGC
                                                                                                                           CGGCGGCTGGCGTCGATGCCGGAGGCCGAACGTCACGAGCATGTCGCCCCGGCTGGTCCGA 411
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48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 37507;
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US-11-075-185-33
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                  545
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                 GGGTGGCCACGACCATCGTCTTCGACCACCCGAC
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TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REPERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
FRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
INUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
SEQ ID NO 33
LENGTH: 3381
TYPE: DNA
ORGANISM: Sorangium cellulosum
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Best Local Similarity
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APPLICANT: JULIEN,
APPLICANT: REID, R
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GGTTGAAATCGCCGATCGCCGTGGAGCTGGGGAGCCCGCCTGGGACGCAGGACACGCCGGA 316
                                               GATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCGGCGGTGACCGGGGTCC
                                                                                                                                      CGGTGCTGGGCCACGCCGACGGTGATCGAGCGTGACGTCGCCTTCCGTGACCTGG
                                                                                                                                                                                      GGCTGTCTCCCGCGCGACGGGAAGAACGGCTGCTCGAATGGGTGCGCGCAGAAATCGCGG
                                                                                                                                                                                                                                  CGATGCCGGAGGCCGAACGTCACGAGCATGTCGCCCGGGCTGGTCCGAGCCGAGGTGGCAG
                                                                                                                                                                                                                                                                               GCGTTGCGCTCGCAGCGTCCAGCATTGCGGAAGAGTCGTGGTCAGAGAAGCTGGCCG
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48.8%;
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Pred. No. 9.8e-07;
0; Mismatches 257;
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AGCTGCCCGTGTCCTTCGTTTACAACCACCCGAC 3197

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US-11-175-689-2
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US-11-254-686-11
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                    APPLICANT: STINEAR, 1
APPLICANT: COLE, STE
APPLICANT: LEADLAY,
APPLICANT: SMALL, EX
APPLICANT: JOHNSON,
APPLICANT: JENKIN,
APPLICANT: DAVIES,
APPLICANT: HAYDOCK,
TITLE OF INVENTION: 1
                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                        Sequence 2, Application US/11175689
Publication No. US20060024806A1
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Matches 177; Conservative
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LENGTH: 1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Burns, Lesley S.
APPLICANT: Graupner, Paul R.
APPLICANT: Lewer, Paul
APPLICANT: Vousden, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/358075
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 62069
CURRENT APPLICATION NUMBER: US/11/254,686
CURRENT FILING DATE: 2005-10-20
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APPLICANT: Waldron, Clive
TITLE OF INVENTION: Novel Spinosyn-Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                           1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 GCGGTTCGTCGAACTGTTCACCGCCGCCGCCGCCGCCGCCCTCTTCGACGAACTCGGTGG 305
                                      STINEAR, TIMOTHY P.
COLE, STEWART T.
LEADLAY, PETER F.
SMALL, PAMELA L.C.
JOHNSON, PAUL D.R
JENKIN, GRANT A.R.
DAVIES, JOHN K.
HAYDOCK, STEPHEN F.
                                                                                                                                                                                                                                                                                                                                                                      GETGGCCACGACCATCGTCTTCGACCACCCGACAGTGGACCGCCTCACCGCGCAC 600
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THE MYCOLACTONE LOCUS: AN ASSEMBLY LINE FOR PRODUCING NOVEL POLYKETIDES, THERAPEUTIC AND PROPHYLACTIC USES
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APPLICANT: GORDON, STEPHEN

APPLICANT: BILLAULT, ALLAIN

ITILE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST

TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED

TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF

TITLE OF INVENTION: MYCOBACTERIA.

FILE REFERENCE: 05344.0011-00000

CURRENT APPLICATION NUMBER: US/10/802,796

CURRENT FILING DATE: 2004-03-18

PRIOR APPLICATION NUMBER: US/09/673,476

PRIOR FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: PCT/1B99/00740

PRIOR APPLICATION NUMBER: DS/060,756

PRIOR PILING DATE: 1998-04-16

PRIOR FILING DATE: 1998-04-16

PRIOR FILING DATE: 1998-04-16

PRIOR FILING DATE: 1998-04-16
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US-10-802-796-658/c
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CURRENT APPLICATION NUMBER: US/11/175,68
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: 10/987,592
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 60/519,864
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-13-14
                                                                                                                                                               SOFTWARE: PatentIn Ver. SEQ ID NO 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 7233
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COLE,
APPLICANT: BUCH
LOCATION: (296)
OTHER INFORMATION: a,
                                         PEATURE: modified_base
                                                                                               ORGANISM: Mycobacterium tuberculosis
                                                                                                                   TYPE: DNA
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                                                                                                                                              LENGTH:
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                                                                                                                                              444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10802796 o. US20050250104A1
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Pred. No. 1.5e-06;
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LOCATION: (314)
OTHER INFORMATION: a,

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NAME/KEY: modified\_base LOCATION: (314)

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PRIOR APPLICATION NUMBER: US/09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 658
LENGTH: 444
TYPE: DNA
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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US-11-221-284-658/c
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Best Local Similarity 53.:
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 658, Application US/11221284
Publication No. US20060063182A1
GENERAL INFORMATION:
                                                                                                                                                                                                                               APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alalin
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REPERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/11/221,284
CURRENT FILING DATE: 2005-09-08
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cole, Stewart APPLICANT: Buchrieser-B
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OTHER INFORMATION: a, t,
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NAME/KEY: unsure LOCATION: (various positions within the sequence) OTHER INFORMATION: applicants are uncertain of bases designated as
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Pred. No. 4.8e-06;
0; Mismatches 122;
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Pred. No. 4.8e-06;
0; Mismatches 122;
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Search completed: April Job time : 228.527 secs 2006, 03:50:14

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: 95

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1280	1038	1569	998	996	1151	932	907	1547	908	886	1009	1007	1003	776	1270	925	1033	935	1088	932	925	Match Length DB	
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CW918299	AG883445	BM542947	CA160031	CNS004NB	CA741271	AG435089	CL507830	AG429738	BQ892601	CL509247	CW938719	AG430654	BU538693	CNS015Y4	CNS017SY	BU531181	AG075627	AG435403	AG392512	BG846745	AG430101	(E) (
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## ALIGNMENTS

ORIGIN	source	FEATURES	COMMENT	JOURNAL	AUTHORS	REFERENCE	ORGANISM	KEYWORDS SOURCE	ACCESSION VERSION	RESULT 1 CNS0091P/c LOCUS DEFINITION
/organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="hacRs19D16" /clone_lib="RPCI-98" /note="end: TET3"	1925	· <	br 131 31000 EVRI CEGEX - FRANCE (E-mail : Begrer@genOSCope.CHS.IY - Web : www.genoScope.chs.fr) Determination of this BAC-end sequence was carried out as part of a	Direct Submission  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :	Genoscope.	<pre>Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 925)</pre>		GSS. Drosophila melanoqaster (fruit fly)	AL053013 AL053013.1 GI:4934461	CNS0091P  925 bp  DNA  linear  GSS 03-JUN-1999  Drosophila melanogaster genome survey sequence TET3 end of BAC #  BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit  fly), genomic survey sequence.

/clone="BACR14B09"

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ACCESSION
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                                                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol type="genomic DNA"
/db_xref="taxon:7227"
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   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanana
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                                                                                                                                                                                                                                                                                                                                            BAC end sequences of Library PTB Unpublished
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes
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                                                                                                                                                                                                                                        Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes
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/note="end : T7"
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30.9%;
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PTB-068F04.R,
                                                                                                                                                                                                                                                                                        Taylor, T.D., Yada, T.,
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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CNS006XK
                                                                                                                         ACCESSION
VERSION
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                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                 UN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC #BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                             GSS
                                                                                                                                   IIY), genomic survey sequence.
AL066051
 Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was generated during the clone tracking errors
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LIBRARY
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/sex="male"
/cell_type="lymphobla:
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 0.00022;
0; Mismatches 258;
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                                                                                                                                                                                                                                                                                           698
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CG756677.1 GI::
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Pristionchus pacificus
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P051-4-D09.zb Ppa BcoRI
Eukaryota; Metazoa; Nematoda; Ch:
Neodiplogasteridae; Pristionchus
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/mal_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR14N09"
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Buntjer, J., van der Meulen, M. and Sommer, R. J.
An integrated physical and genetic map of the nematode I
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial RCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fly), genomic survey sequence.
AL053013
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BP 191 91006 EVRY cedex - FRANCE (

    Web : www.genoscope.cns.fr)

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CCSYSYSSSTSSSSTSWGSTSGSSSSSSYGTSGSSDSTSTCCSCCCYMCTCCSTYBMBCY
                                                                                                                                                                                             TCCGTGACCTGGGATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCGGCGG
                                                                                                                                                                                                                                                            CCGAGGTGGCAGCGGTGCTGGGCCACGGCACGCCGACGGTGATCGAGCGTGACGTCGCCT
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                                                                  TGACCGGGGTCCGGGTGGCCACGACCATCGTCTTCGACCACCCGACAGTGGACCGCCTCA
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/clone_lib="RPCI-98"
/note="end : TET3"
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/mol_type="genomic_DNA"
/db_xref="_axon:7227"
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Pred. No. 0.00066;
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(E-mail :
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RESULT 7
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AUTHORS
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Best Local Similarity
Matches 232; Conserv
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TITLE
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                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17.NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 17-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC (library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, Tsukuba Institude of Physical and Chemical Research (RIKEN) 3-1-1 Phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp
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R.Site
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LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shiroishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Bzawa,K., Saitou,N., Hattori,M., Sakaki,Y.,
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ACCCGCAGCGGGCGATCGAGGAGCTGCGGGACCCCTGGACGCCGGGGGACCCGTGGGTGT 223
                                                           AGAACATGGCCGGTACCGAGGGCGGCGACTACCTGCGCAGCCAGGGCCTGCGCGCCATGG
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                               clone="MSMg01-193C09.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus molossinus"
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45.7%;
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Pred. No. 0.00065;
0; Mismatches 276
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clone:MSMg01-193C09.T7, genomic
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Moriwaki, K.
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RESULT 8
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AUTHORS
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Query Match
Best Local Simi
Matches 168;
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                                                                                                                                                                                                                                                                   Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-UUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS010RY 776 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN04P24 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence.
AL099352
AL099352.1 GI:5610963
GSS.
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                    Similarity
                                                                                                                                                                                                                                                        pBeloBAC11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCGGCGGTGACCGGGGTCCGGGTGGC 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTCCGAGCCGAGGTGGCAGCGGTGCTGGGCCACGGCACGGTGATCGAGCGTG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTGGTGGACCTGGACCGGGAGCGGTTCGTCGAACTGTTCACCGCCGCCGCCGCCGGC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                       /clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                            /organism="Drosophila melanogaster"
/mal_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN04P24"
                                                                                                                                                                                                                                     Location/Qualifiers
57;
Score 69.6; DB 10;
Pred. No. 0.00079;
7; Mismatches 221;
 Indels
                                  Length
0
Gaps
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIN
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.B. Consortium/LLNL at:
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Location/Qualifiers
/tissue type="normal pigmented retinal epithelium"
/lab host="NIH MGC 43"
/clone_lib="NIH MGC 43"
/clone_gan: eye, Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye, Vector: poTB7; Site_1: XhoI; Site_2: XhoI
                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
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Best Local Similarity 44.3%;
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Pred. No. 0.00078;
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1007 bp AGENCOURT\_8298624 NIH\_MGC\_100 Ho 5', manA sequence. BQ650254 BQ650254.1 GI:21774426 EST. Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: CGAP (Stanford) 1 (bases 1 to 1007)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999) found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2445 row: o column: 15 Eukaryota; Metazoa; Mammalia; Eutheria; Hominidae; Homo domo sapiens (human) cDNA Library Preparation; Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can quality sequence stop: Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homo mRNA sapiens Gene linear EST 15-JUL-2002 CDNA clone IMAGE:6270566 Collection (MGC) þ,

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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 100"
/clone lib="NIH MGC 100"
/clone correction of the correction o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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AZ196424 886 bp DNA linear GSS 31-AU SP 103, AL AUS_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpurat genomic clone Plate=1032 Col=9 Row=A, genomic survey sequence AZ196424 AZ196424 AZ196424 1 GI:8390247 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS.
Drosophila melanogaster

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out

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Direct Submission
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1 (bases 1 to 1009)
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/db_xref="taxon:7227"
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Pred. No. 0.0011;
7; Mismatches 167;
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Buechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Swartzell,S., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7
Class: BAC end
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Plate: 1032 row: A column:
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California Institute of Technology
Pasadena California 91125, USA
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A sea urchin genome project: Sequence scan,
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(626) 793-3047
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llarity 46.7%;
Conservative
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|mol_type="genomic DNA"
|mol_type="genomic DNA"
|db_xref="ftaxon:7668"
|clone="plate=1032 Col=9 Row=A"
|clone=1bl="Strongylocentrotus purpuratus, purple se
urchin, sperm genomic BAC library"
|note="Organ: sperm; Vector: BACe3.6; BAC Clones in
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Pred. No. 0.0018;
0; Mismatches 26
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Tel: 49 221 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: savard@uni-koeln.de
Class: BAC ends.
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Fax: 49 221 470 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Savard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neoptera; Endopterygota;
Tenebrionidae; Tribolium.
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Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
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Similarity 47.5%;
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/mol_type="genomic DN
/strain="GA-2"
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ezawa, K.,
Shiroishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1547)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 14 (12),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing : TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus molossinus (Japanese wild mouse) Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence-SNP analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                      969 939 Physical description of the properties o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="MSMg01-176J21.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="male"
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Pred. No. 0.00
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clone:MSMg01-176J21.TJ, genomic survey
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Moriwaki, K.
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grossman,A., Davies,J., Rederspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardti Genome: A Model, Unicellular System for Analyzing Gene Punction and Regulation Unicellular System for Analyzing Gene Punction and Regulation Unicellular Plants; project phase 2
                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 919 613 8159 Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1024012H11.yl C. reinhardtii CC-1690, normaliz
Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duke University
Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                              chauser@duke.edu.
mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene)
                                                                                                                                                             /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                                                                                                                                                          /strāin="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                           organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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phage. The library was normalized using method 4 described
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3CGGCGCGGCCGCGGGCGCGCGCG 426	485 GGCCGCGGGCGCCGCGCGCGCGGGGGGCGCGCGCGCGC	DP.
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ccaccaccacacacccccaccaccac	545 caccadacadcadcadacadcadcadacadacadacada	Dp.
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GCGCGGGCGCCGCACCGCCCGGCACCGCC 546	605 GCGCGGCGCCCCCGGCGCCCCCCGCCGCGCGCGCGCGC	Db 6
CCGCCGCCGGCCCTCTTCGACGAACTCG 301	242 GGGAGCGGTTCGTCGAAACTGTTCACCGCCGCCCGCCGGCCG	8
recccegeagregageccecececece 606	665 GCGCCGGGCCCGCCGCGGGGGGGGGGGGGGGGGCCCGCGC	Db 6
CCCGTGGGTGTCGGTGGTGGACC 241	182 AGGAGCTGCGGACCACCCTGGACGCCGGGGGACCCCTGGGACCTGGACCTGGACC	97
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ceeseceeseersereceeseesees 786	845 CCACCGCCGCCCCGCCCACGCCCACCGCCCCCCCCCCC	Db 8
CGCCTTCGCCCGTCGTCGGCGCAGTG 61	2 CCTCCTACGCGGGGGAAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGTG	S.
65.4; DB 2; Length 907; No. 0.0053; mmatches 312; Indels 3; Gaps 2;	10.9%; Score Similarity 46.6%; Pred. 5; Conservative 0; Mil	Query Match Best Local Matches 27
Genome Research 6: 791-806."	in bonaldo et al (1996) Genome kesearch	ORIGIN

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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## ALIGNMENTS

US-10-611-442-2

APPLICANT: Hutchinson, C. Richard
APPLICANT: Katz, Leonard
APPLICANT: Reid, Ralph
APPLICANT: Hu, Zhihao
APPLICANT: Hu, Zhihao
APPLICANT: Gramajo, Hugo
TITLE OF INVENTION: RECOMBINANT GENES FOR POLYKETIDE
TITLE OF INVENTION: MODIFYING ENZYMES
FILE REFERENCE: 300622009100
CURRENT APPLICATION NUMBER: US/10/611,442
CURRENT PILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 60/393,016
PRIOR APPLICATION NUMBER: US 60/393,016
PRIOR PILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 24
SEQ ID Query Match 100.0%; Score 601; DB 8; Best Local Similarity 100.0%; Pred. No. 1e-138; Matches 601; Conservative 0; Mismatches 0; Sequence 2, Application US/10611442 Publication No. US20040203015A1 GENERAL INFORMATION: FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Genomic DNA

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1200 GCCTCCTACGCGGCGACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT 1259

1 GCCTCCTACGCGGCGGCAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT 60

Length 17596; Indels 0;

Gaps

1260 GGGCTGCCGGTCACCTCGATCGCCTGGGGTTCTGTGGGCCGGGCAGAACATGGCCGGTACC

GAGGGCGGCGACTACCTGCGCAGCCAGGGGCCTGCGCGCCATGGGACCCGCAGCGGGCGATC 180

1379

1319

61 GGGCTGCCGGTCACCCTCGATCGCCTGGGGTCTGTGGGCCCGGGCAGAACATGGCCCGGTACC 120

181 GAGGAGCTGCGGACCACCCTGGACGCCGGGGACCCCGTGGGTGTCGGTGGTGGACCTGGAC 240

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APPLICANT: SANTI, DANIEL V.
APPLICANT: REID, RALPH C.
APPLICANT: KODUMAL, SARAH J.
APPLICANT: JAVARAJ, SEBASTIAN
TITLE OF INVENTION: SYNTHETIC GENES
FILE REPERENCE: 300622010900
CURRENT APPLICATION NUMBER: US/10/672,396
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 60/414,085
PRIOR APPLICATION NUMBER: US 60/414,085
PRIOR FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR T
FILE REFERENCE: 3016-2US
CURRENT APPLICATION UMBER: US/10/205,032
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 39
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SEQ ID NO 17
LENGTH: 4725
TYPE: DNA
ROGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-17
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US-10-205-032-17
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Best Local Similarity
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APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLS OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
FILE REFERENCE: 3016-2US
CURRENT APPLICATION UNMBER: US/10/205,032
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: micromonospora carbonacea subspecies aurantiaca
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Pred. No. 3e-45;
0; Mismatches 228;
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; TYPE: DNA; ORGANIAM: Streptomyces avermitilis; ORGANIAM: Streptomyces avermitilis; PEATURE: ; NAMB/KEY: CDS; LOCATION: (11...(18438))
US-10-156-761-2886
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-05
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SEQ ID NO 2886
LENGTH: 18438
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
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Local Similarity 61.3%;
181 GAGGAGCTGCGGACCCTGGACGCCGGGGACCCGTGGGTGTCGGTGGTGGACCTGGAC
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Pred. No. 1.2e-42;
0; Mismatches 220; Indels 6
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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US-10-156-761-15102
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 15102
LENGTH: 125746
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                          GACCTGGCGCGGGACCTCGCCCCGCGGCGGGGGGGGCGCTCGATGGACCCGGGACCGGGCGATC
                                                                                                                                                      GGCCTCACCGCCACCTCCGTGGCCTGGGGCAGCTGGGCCGGCGGGGGATGGTCGACGAC
                                                                                                                                                                                GOGCTGCCGGTCACCTCGATCGCCTGGGGGTCTGTGGGCCGGGCAGAACATGGCCCGGTACC
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GGCGCGCTCCAGCAGGCCCTCGÁCCACGACGAGGCCACGCTGACGGTCACCGÁCATGGÁC
                                  GAGGAGCTGCGGACCACCCTGGACGCCGGGGACCCGTGGGTGTCGGTGGTGGACCTGGAC 240
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HORIKAWA, HIROSHI
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Pred. No. 8.4e-43;
0; Mismatches 220; Indels 6;
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US-10-156-761-1/c
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Best Local Similarity
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                                                                                                                                                                          3615065 GGCGCGTACGCGGCCGACGCGTACGCCGACGCGCTCGCGGCGGACCGGCGCAGGCGC
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                    GACCTGGCGCGGGACCTCGCCCGCGGGGGGGGGTGCGCTCGATGGACCCGGGACCGGGCGATC
                                                          GAGGGCGACTACCTGCGCAGCCAGGCCTGCGCGCCATGGACCCGCAGCGGGCGATC
                                                                                                GGCCTCACCGCCACCTCCGTGGCCTGGGGCAGCTGGGCCGGCGGCGGGATGGTCGACGAC
                                                                                                                                | GGGCTGCCGGTCACCTCGATCGCCTGGGGGTCTGTGGGCCGGGAGAACATGGCCGGTACC
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Sequence 1, Application US/10156761 Publication No. US20030119018A1
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                                                                                                                                                                                                                   ACCGGCGTACGTCTGCCCGCCACGCTCGTCTTCGACCACCCCAC
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                                                                                                                                                                                                                          37177
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SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
CORGANISM: Streptomyces avermitilis
PEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other
US-10-156-761-1 APPLICANT: INLOWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02 APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO APPLICANT: ISHIKAWA, JUN APPLICANT: HORIKAWA, HIROS APPLICANT: SHIBA, TADAYOSH NUMBER OF SEQ ID NOS: 15109 other or unknown

34.9%;

0

Score 210; DB 6; Length 90 Pred. No. 3.6e-43; 0; Mismatches 220; Indels

Length 9025608;

6 Gaps

180

3614946

3614886

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APPLICANT: Bachmann, Brian O.
APPLICANT: Piraee, Mahmood
ITITLE OF INVENTION: POLYEME POLYKETIDES, PROCESSES FOR THEIR PRODUCTION AND THEIR USE
ITITLE OF INVENTION: PHARMACEUTICALS
FILE REFERENCE: 3004-9US
CURRENT APPLICATION NUMBER: US/10/760,493
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: USSN 60/441,123
PRIOR APPLICATION NUMBER: USSN 60/441,123
PRIOR APPLICATION NUMBER: USSN 60/469,810
PRIOR FILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: USSN 60/469,810
PRIOR APPLICATION NUMBER: USSN 60/491,516
PRIOR APPLICATION NUMBER: USSN 60/494,568
PRIOR PILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR PILING DATE: 2003-08-01
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US-10-760-493-34
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                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ecopia BioSciences Inc
APPLICANT: Farnet, Chris M.
APPLICANT: MCALpine, James B.
APPLICANT: Zazopoulos, Emmanuel
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn
                                                                                                                                                                                                                                                              LENGTH: 9684
TYPE: DNA
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                                                                                                                                                                      Similarity
                                                                                             GCCTCCTACGCGGCGAGCAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT
                                      GGGCTGCCGGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGGCAGAACATGGCCGGTACC 120
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                 version 3.0
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                                                                                                                                                                Score 207.6; DB 9; Pred. No. 5.4e-42;
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                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/760,493
CURRENT FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: USSN 60/441,123
PRIOR FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: USSN 60/469,810
PRIOR PILING DATE: 2003-05-13
PRIOR PILING DATE: 2003-08-01
PRIOR PILING DATE: 2003-08-01
PRIOR PILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: USSN 60/494,568
PRIOR APPLICATION NUMBER: USSN 60/494,568
PRIOR APPLICATION NUMBER: USSN 60/494,568
PRIOR PILING DATE: 2003-08-13
NUMBER OF SEQ ID NOS: 78
SOPTWARE: Patentin version 3.0
SEQ ID NO 18
                                                                      ; LENGTH: 164051
; TYPE: DNA
; ORGANIZM: Streptomyces alzunensis
US-10-760-493-18
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US-10-760-493-18
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 Query Match
Conservation
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Best Local Sin
Matches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bachmann, Brian O.
APPLICANT: Piraee, Mahmood
TITLE OF INVENTION: PHARMACEUTICALS
TITLE OF INVENTION: PHARMACEUTICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ecopia BioSciences Inc
APPLICANT: Farnet, Chris M.
APPLICANT: McAlpine, James B.
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 Conservative
               34.5%; Score 207.6; DB 9; 60.3%; Pred. No. 3.1e-42;
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0; Mismatches
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CCCGAGGCGCGGGAGGTCATGGACGCCACGCGCACGGAGGAGGACACCGGCAGC 4413
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US-10-205-032-19
; Sequence 19, Application US/10205032
; Publication No. US20030113874A1
; GENERAL INFORMATION:
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; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-19
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CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 5355
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 359; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR
FILE REFERENCE: 3016-2US
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PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: 60/553,384
PRIOR FILING DATE: 2004-03-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Versior
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10937730A Publication No. US20050112726A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sin Matches 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HU, Zhihao
APPLICANT: REID, Ralph
TITLE OF INVENTION: Biosynthetic Gene Cluster
FILE REFERENCE: 010092.02
CURRENT APPLICATION NUMBER: US/10/937,730A
CURRENT FILING DATE: 2004-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 67167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 33.5%;
Local Similarity 59.6%;
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    GAGGGCGGCGACTACCTGCGCAGCCAGGGCCTGCGCGCCATGGACCCGCAGCGGGCGATC
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                                                                                                   GGGCTGCCGGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGGCAGAACATGGCCGGTACC
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Pred. No. 1.1e-40;
0; Mismatches 239;
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Gaps

120 62691 60

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APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Bachmann, Brian O.
APPLICANT: Bachmann, Brian O.
APPLICANT: Piraee, Mahmood
TITLE OF INVENTION: POLYENE POLYKETIDES, PROCESSES FOR THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PHARMACEUTICALS
FILE REFERENCE: 3004-9US
CURRENT APPLICATION NUMBER: US/10/760,493
CURRENT FILING DATE: 2004-01-21
FRIOR APPLICATION NUMBER: USSN 60/441,123
PRIOR FILING DATE: 2003-05-13
PRIOR FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: USSN 60/469,810
PRIOR APPLICATION NUMBER: USSN 60/491,516
PRIOR FILING DATE: 2003-08-13
PRIOR APPLICATION NUMBER: USSN 60/491,516
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-01
PRIOR FILING DATE: 2003-08-13
 S
                                                                                                ; TYPE: DNA ; ORGANISM: Streptomyces aizunensis US-10-760-493-22
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US-10-760-493-22
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APPLICANT: Ecopia BioSciences Inc
APPLICANT: Farnet, Chris M.
APPLICANT: McAlpine, James B.
APPLICANT: Zazopoulos, Emmanuel
                                                  Query Match
Best Local (
                                                                                                                                               SEQ ID NO 22
LENGTH: 24444
                                 Matches 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Appropriate Publication No.
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn versi
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                                                 Similarity
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No. US20050187167A1
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                                Conservative
                                                                                                                                                                            version 3.0
                                               33.1%;
                              Score 199; DB 9; Length 24.
Pred. No. 5.9e-40;
0; Mismatches 220; Indels
                                                            Length 24444;
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; LOCATION: (1)...
US-10-156-761-412
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                                                                                                                                                          PRIOR FILING DATE: 2001-08-
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 412
LENGTH: 18435
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                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILB REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                          TYPE: DNA
ORGANISM: Streptomyces
FEATURE:
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FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 15103
LENGTH: 100000
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Best Local Similarity
Matches 378; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15103, Application US/10156761 Publication No. US20030119018A1
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APPLICANT: OMURA, SATOSHI
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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Pred. No. 8.8e-40;
0; Mismatches 221;
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US-10-156-761-411
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  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
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Best Local Simi
Matches 378;
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSI
APPLICANT: SAKAKI, YOSHIYI
                                                                                                                                                                                                                                                                                                                         Sequence 411, Application US/10 Publication No. US20030119018A1 GENERAL INFORMATION:
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Similarity 60.4%;
78; Conservative
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; LENGTH: 10056
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis FEATURE:
; PEATURE:
; NAME/KEY: CDS
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ION: (3462) INFORMATION:	EY: CDS INFORMATION: (2072) INFORMATION: INFORMATION: INFORMATION: INFORMATION:	BY: CDS ON: (928) INFORMATION: INFORMATION:	PEATURE: MICLOMOLOGEOIA PEATURE: NAME/KEY: CDS LOCATION: (1)(144) COTHER INFORMATION: megBV: OTHER INFORMATION: CEO II	1	FILING DATE: 2000- FILING DATE: 2000- OF SEQ ID NOS: 34		PAR.	GENERAL INFORMATION: APPLICANT: WcDaniel, APPLICANT: Volchegur TITLE OF INVENTION: TITLE OF INVENTION:	9-1 , Applica		222	222	23	23	222	222	2334	225	<b>у</b>
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Y), mycaro O: 5= tran deoxysugar to-6-deoxy O: 6= tran	NO: 3= trans rhodosaminyl osamine glycono: 4= trans	der der	(megT), TD		8 7		(O)	ு நட்	5792		222	999	ជ្ជ ជ	555	999	gg	999	999	<b>‡</b>
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NAME/KEY: misc feature
LOCATION: (17155)...(17694)
OTHER INFORMATION: megAI, KRI
NAME/KEY: misc feature
LOCATION: (17947)...(18207)
OTHER INFORMATION: megAI, ACPI
NAME/KEY: misc feature
IOCATION: (24544)...(25581)
OTHER INFORMATION: megAII, AT3
NAME/KEY: misc feature
LOCATION: (26230)...(26733)
OTHER INFORMATION: megAII, KR3 (:
NAME/KEY: misc_feature
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LOCATION: (6592)...(7197)
OTHER INFORMATION: megDIV,
OTHER INFORMATION: SEQ ID:
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LOCATION: (10483)...(11424)
OTHER INFORMATION: megBIV, TDP-hexose 4-ketoreductase,
OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 4-ketoreductase;
OTHER INFORMATION: SEQ ID NO: 12= translated amino acid sequence
NAME/KEY: CDS
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LOCATION: (9226)...(10479)
OTHER INFORMATION: megBV, mycarosyl transferase, mycarose glycosyltransferase;
OTHER INFORMATION: SEQ ID NO: 11= translated amino acid sequence
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LOCATION: (7220)...(8206)
OTHER INFORMATION: TDP-4-1
OTHER INFORMATION: TDP-4-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (19876)...(20910)
OTHER INFORMATION: megAI, AT2
NAME/KEY: misc feature
LOCATION: (215T)...(22053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (15427)...(16476)
OTHER INFORMATION: megAI, ATI
                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (22957)...(24237)
OTHER INFORMATION: megAII, KS3
NAME/KEY: misc feature
                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (22867)...(33555)
OTHER INFORMATION: megAII; SEQ ID NO: 14= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (22318)...(22575)
OTHER INFORMATION: megAI, ACP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (13576)...(13791)
OTHER INFORMATION: megAI, ACP-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (12181)...(22821)
OTHER INFORMATION: megAI; SEQ ID
NAME/KEY: misc_feature
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OTHER INFORMATION: megAI, KR2
NAMR/KRY: miso forture
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LOCATION: (13849)...(15126)
OTHER_INFORMATION: megAI, KS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (12505)...(13470)
OTHER INFORMATION: megAI, AT-L
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OTHER INFORMATION: megAI, KS2
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TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SEQ ID NO NO: 9= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose
SEQ ID NO: 10= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      megDIV, TDP-4-keto-6-deoxyglucose 3,5-epimerase TDP-4-keto-6-deoxyhexose 3,5-epimerase; SEQ ID NO: 8= translated amino acid sequence
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O: 7= translated amino acid sequence
                             (inactive)
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Matches 601; Conservative 0;
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LOCATION: (29953)...(30477)
OTHER INFORMATION: megAII, DH4
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LOCATION: (28897)...(29931)
OTHER INFORMATION: megAII, AT4
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LOCATION: (42168)...(42425)
OTHER INFORMATION: megAIII,
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LOCATION: (41406)...(41936)
OTHER INFORMATION: megAIII,
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LOCATION: (39795)...(40811)
OTHER INFORMATION: megAIII,
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OTHER INFORMATION: megAIII,
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OTHER INFORMATION: megAIII,
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OTHER INFORMATION: megAIII,
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LOCATION: (35385)...(36419)
OTHER INFORMATION: megAIII,
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OTHER INFORMATION: megAIII,
NAME/KRY. mion fortune
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OTHER INFORMATION: megAIII;
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OTHER INFORMATION: megali,
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LOCATION: (33052)...(3
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OTHER INFORMATION: megAII,
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LOCATION: (32257)...(3
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OTHER INFORMATION: megAII, ER4
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LOCATION: (4258
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LOCATION: (38187)...(3
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LOCATION: (33780)...(3
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LOCATION: (31396)...(3)
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                                                                                       (47411)...(47980)
RMATION: megF, C-6 hydroxylase; SEQ
                                                                                                                                                                                                                                                                  (45620) . . . (46591)
                                                                                                                                                                                                                                                                                                     (44355)...(45623)
RMATION: megCIII,
RMATION: SEQ ID N
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                                                                                                                                                                         (46660) . . . (47403)
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N: megAIII,
                                                                                                                                                                                                                               megBII-2(megBII), TDP-4-keto-6-deoxy-L-glucose
TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
                                                                                                                                                                                                                                                                                                                                                                               megCII, TDP-4-keto-6-deoxyglucose 3,4-isomerase, SEQ ID NO: 16= translated amino acid sequence
                                                                                                                                                 megH, TEII;
                                                                                                                                                                                                           SEQ ID NO: 18=
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O: 17= translated amino acid sequence
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 Score 601; DB 3;
Pred. No. 2.5e-104;
; Mismatches 0;
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8= translated amino
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                                      Length 47981;
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CLASSIFICATION:

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RESULT 2
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                                                                                                                                                                                                                 Sequence 3, Application US/07642734C
Patent No. 5824513
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Mcalpine, J
TITLE OF INVENTION: Recombinant DNA Method for Producing TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                  ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 4.
          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/642,734C
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STREET:
CITY: Ab
FILING DATE:
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Abbott Laboratories D377/AP6D-2 One Abbott
Park Rd
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LOCATION: 4471.5847
OTHER INFORMATION: /funct
OTHER INFORMATION: beta-k
PEATURE:
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LOCATION: 3406.3921
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4171.4428
OTHER INFORMATION: /func
OTHER INFORMATION: acyl
FEATURE:
NAME/KEY: misc_feature

NAME/KEY: misc_feature
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NAME/KEY: misc feature
LOCATION: 1693..2670
OTHER INFORMATION: /func
OTHER INFORMATION: acylt
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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LOCATION: 19.4470
OTHER INFORMATION: /func
OTHER INFORMATION: modul
PEATURE:
NAME/KEY: misc_feature
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LOCATION: 19..10722
OTHER INFORMATION: /c
OTHER INFORMATION: /f
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OTHER INFORMATION: /p
FEATURE:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952.US.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                      FEATURE:
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TYPE: nucleic
STRANDEDNESS:
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LOCATION: 4471..10722
OTHER INFORMATION: /fur
OTHER INFORMATION: modu
NAME/KEY: misc feature
LOCATION: 7165.9216
OTHER INFORMATION: /fur
OTHER INFORMATION: dehy
                                                                                     NAME/KEY: misc feature LOCATION: 6054.7026 OTHER INFORMATION: /fur OTHER INFORMATION: acy:
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module 3"
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beta-ketoacylACPsynhase domain of module"
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beta-ketoreductase domain of module 3"
   dehydratase
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acyltransferase domain module
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beta-ketoacyl ACP synthase of
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3
6-deoxyerythronolide B"
/function= "approximate span of
dehydratase and enoylreductase
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CATION: misc feature

CATION: 14857..15114

OTHER INFORMATION: /functic

OTHER INFORMATION: acyl car

FEATURE:

NAME/KEY: misr

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FEATURE: misc feature
LOCATION: 10831.12174
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
OTHER INFORMATION: beta-
FEATURE: misc feature
LOCATION: 12379.13350
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OTHER INFORMATION: /func
OTHER INFORMATION: /prod
OTHER INFORMATION: 6-deo
FEATURE:
NAME/KEY: misc feature
LOCATION: 10723..15165
OTHER INFORMATION: modul
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NAME/KEY: misc feature
LOCATION: 18379..18921
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
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LOCATION: 15166.20235
OTHER INFORMATION: /func
OTHER INFORMATION: modul
FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..16569
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OTHER INFORMATION: /func OTHER INFORMATION: acyl FEATURE:
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NAME/KEY: misc feat:
LOCATION: 10225..10
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /func
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 14062..14610
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LOCATION: 9433.9984
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OTHER INFORMATION: bet
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N: 10723..20235

NFORMATION: /codon start= 10723

INFORMATION: /function= "gene =eryA"

INFORMATION: /product= "orf3 encoding modules 5 / Property of the start of the sta
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acyl carrier domain of module 5"
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beta-ketoacylACPsynthase domain
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acyl carrier domain of module 4"
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beta-ketoacylACPsynthase domain of modul"
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beta-ketoreductase domain of
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beta-ketoreductase of module
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chioesterase domain of module 6"
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Sequence 3, Application US/08439009A
Patent No. 6004787
GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Katz, L
APPLICANT: Mealpine, J
APPLICANT: Mealpine, J
TITLE OF INVENTION: Specific Polyk
NUMBER OF SEQUENCES: 27
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Best Local 9
                                                                                                                                                 NUMBER OF THE TOTAL OF T
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                     STATE: I
                                                                                                                                    STREET:
                                                                           ZIP: 60064-3500
                                                                                                                       CITY: Abbott Park
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78.9%;
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Specific Polyketides
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Pred. No. 3.3e-66;
0; Mismatches 127;
   Version #1
                                                                                                                                                                                                                                 Biosynthesis
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435

US/08/439,009A

ATTORNEY/AGENT INFORMATION:

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LOCATION: 19.4470
OTHER INFORMATION: /function= "a OTHER INFORMATION: module 3"
FEATURE: MAME/KEY: misc feature
LOCATION: 97. 7^^^
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OTHER INFORMATION: /funct
OTHER INFORMATION: beta-k
FEATURE:
                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /func:
OTHER INFORMATION: acyl:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4471..10722
OTHER INFORMATION: /func:
OTHER INFORMATION: moduli
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NAME/KEY:
LOCATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sacch
                                                  NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module
FEATURE:
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NAME/KBY:
LOCATION:
                                                                                                                       PEATURE:
NAME/KBY:
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LOCATION: 19.10722
OTHER INFORMATION:
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                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 4471..5847 OTHER INFORMATION: /fur OTHER INFORMATION: beta
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: 3406.3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: 1693..2670 OTHER INFORMATION: /fur OTHER INFORMATION: acyl
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STRAIN: NRRL 238
   OTHER INFORMATION:
                    NAME/KBY:
LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US
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                  misc_feature
7165..9216
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beta-ketoacylACPsynhase
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acyl carrie
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acyltransferase domain module 3"
                                                                                                                                                                                                                                                   /function=
module 4"
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4
6-deoxyerythronolide B"
/function= "approximate span of
                                                                                                                                                                                                                                                                                                                                         ction= "approximate span of carrier domain of module 3"
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LOCATION: 12379..13350
OTHER INFORMATION: /funct
OTHER INFORMATION: acyltr.
FEATURE:
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OTHER INFORMATION: /funct
OTHER INFORMATION: module
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 14857..15114
OTHER INFORMATION: /func
OTHER INFORMATION: acyl
FEATURE:
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                       FEATURE:

NAME/KEY: misc_feature

TOTATION: 19492..20235
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FRATURE:
NAME/KEY: misc feature
LOCATION: 9433.9984
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: 16768..17721 OTHER INFORMATION: /fur OTHER INFORMATION: acyl
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LOCATION:
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LOCATION: 19149..19398
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
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 INFORMATION:
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18379..18921
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acyltransferase domain of module
                                                                                      acy1
                                                                                                                                                                                                                                                                                                                                                                                                                                   module
/function= "approximate span of
thioesterase domain of module 6"
                                                                                                                                                                       /function= "approximate span beta-ketoreductase domain of
                                                                                                                                                                                                                                                                                                                                              /function= "approximate span of
beta-ketoacylACPsynthase domain
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beta-ketoreductase of module
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/function= "gene =eryA"
/product= "orf3 encoding modules
6-deoxyerythronolide B formatio"
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acyl carrier domain of module
                                                                                    /function= "approximate span c
acyl carrier domain of module
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US-07-642-734C-1
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Best Local
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                                                                                                                                                                                                                                                                                          Sequence 1, Application US/07642734C Patent No. 5824513
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                          APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Recombinant DNA Method
TITLE OF INVENTION: Erythromycin Analogs
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                   COUNTRY: US
ZIP: 60064-3500
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Abbott Park
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                                                                                                                                 Abbott Laboratories D377/AP6D-2 One
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78.9%;
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Pred. No. 3.3e-66;
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ORGANISM: Saccharopolyspora e.
STRAIN: NRRL 2338
FEATURE: NRRL 2338
FEATURE: MISC_feature
LOCATION: 744.6659
OTHER INFORMATION: /function=
OTHER INFORMATION: /label= FUN
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SOFTWARE: PATENTIN Releac
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 17-JAN-91
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NAME/KEY: misc feature
LOCATION: 744...1868
OTHER INFORMATION: /funct
OTHER INFORMATION: acyltr
FEATURE:
NAME/KEY: misc feature
LOCATION: 1998...2198
OTHER INFORMATION: /funct
OTHER INFORMATION: acyl c
                                NAME/KEY: misc feature
LOCATION: 6369.6626
OTHER INFORMATION: /func
OTHER INFORMATION: acyl
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678.11219
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sacch
                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 5574..6125
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module
FEATURE:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 2250..3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3831..4811
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NAME/KEY:
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LOCATION: 744..11219
COTHER INFORMATION: /function= "gene= "eryA""
OTHER INFORMATION: /product= ""ORF1 encoding modules 1 & 2
OTHER INFORMATION: 6-deoxyerythronolide B""
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STRANDEDNESS: doub
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LOCATION: 6678..11
OTHER INFORMATION:
OTHER INFORMATION:
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n Release #1.0, Version #1.25
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  /function= "approximate span
module 2"
                                                                                                   /function= "approximate span of acyl carrier domain 2 of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= "approximate span of
acyl carrier domain 1 of module
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NAME/KEY:
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LOCATION:
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LOCATION: 10707..10964
OTHER INFORMATION: /function= "approximate
OTHER INFORMATION: acyl carrier domain of n
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LOCATION: 9906..10454
OTHER INFORMATION: /fw
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                                                               ACCGGGCTCCGCCTCGACGCTGGTCTTCGACCACCCGAACGCCTCCGCGGTCGCC 10943
                                                                                       ACCGGGGTCCGGGTGGCCACGACCATCGTCTTCGACCACCCGACAGTGGACCGCCTCACC
                                                                                                                               AAGGAGCTCGGGTTCGACTCGCTGGCGGCCGTCCGGCTGCGCAACCTGCTCAACGCGGCC 10883
                                                                                                                                                     CGTGACCTGGGATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCGGCGGTG 534
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8262..9305
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6678..8066
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Pred. No. 1.4e-29;
0; Mismatches 229;
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RESULT 5 US-08-439-009A-1 ; Sequence 1, Application US/08439009A

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IOCATION: 744.7659

OTHER INFORMATION: MODULE
OTHER INFORMATION: MODULE
OTHER INFORMATION: /label
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GENERAL INFORMATION:
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OTHER INFORMATION: /fic
OTHER INFORMATION: /pu
OTHER INFORMATION: 6-
FEATURE:
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FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis
TITLE OF INVENTION: Specific Polyketides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,
                                                                                                                  FEATURE
                                                                                                                                                                                                 FEATURE:
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LENGTH: 11219 base pai
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LOCATION:
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OTHER
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STREET:
CITY: Ab
                                              NAME/KEY: misc feature
LOCATION: 2250..3626
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
                                                                                                                            NAME/KEY: misc feature LOCATION: 1998..2198 OTHER INFORMATION: /fur OTHER INFORMATION: acyl
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STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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TYPE: nucleic acid
STRANDEDVESS: double
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                                                                                                                                                                                                             /KEY: misc_feature
TION: 744..1868
R INFORMATION: /func
R INFORMATION: acyli
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Abbott Laboratories D377/AP6D-2 One
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misc_feature
3831..4811
                                            /function= "approximate span of
beta-ketoacylACP synthase domain/module1"
                                                                                                                               acy1
                                                                                                                                                                                                             /function= "approximate span acyltransferase domain 1 of \pi
                                                                                                                                                                                                                                                                                               /function= "gene= "eryA""
/product= ""ORF1 encoding modules 1 & 2
6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                               /function= "APPROXIMATE SPAN MODULE 1" /label= FUNCTION
                                                                                                                              /function= "approximate | acyl carrier domain 1 of
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NAME/KEY:
LOCATION:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION: /fur
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NAME/KEY: misc_feature
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LOCATION: 9906...10454
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module
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LOCATION: 8262..9305
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LOCATION: 10707..10964
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GAGGTGGCAGCGGTGCTGGGCCACGGCACGGTGATCGAGCGTGACGTCGCCTTC
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                                                                                                                                  ATCGTCACGACCGCGCGAGCGAGCGGGCCGGAGAACCGGAGACGGAGAGCCTGCGCGAC 10703
                                                                                                                                                                     CTCGGTGGGGTCCGCGCGGGGCCGAGGAGGAACCGGTCAGGAATCGGGATCTCGCCCG---G
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                                                                                                                                                                                                                                                                                   ATCGAGGAGCTGCGGACCACCCTGGACGCCGGGGGACCCCGTGGGTGTCGGTGGGACCTG
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                                                              CGGCTGGCGGGTCTGCCGCGTGCCGAGCGGACGGCGGAGCTGGTGCGCCCTGGTCCGCACC 10763
                                                                                            CGGCTGGCGTCGATGCCGGAGGCCGAACGTCACGAGCATGTCGCCCGGCTGGTCCGAGCC 414
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6369..6626
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acyl carrier domain of module 2"
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acyltransferase 2 domain of module 1"
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module 2"
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beta-ketoacyl ACPsynthase of
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module
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                                                                   Query Match
Best Local Sim:
Matches 361;
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Patent No. 614352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Baltz, Richard
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                             TELEFAX: (317)337-484'
                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Tunner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                              TELEPHONE: (31/)37-4847
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Indianapolis
STATE: Indiana
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GGCGCTTACGGCGCGGCGAACGCATTCTTGGACACACTCGCCGAACAACGCCGAGCACGC 39480
                       GCCTCCTACGCGGCGGCAACGCCTTCCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT 60
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9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broughton, Mary C. Crawford, Kathryn P. Madduri, Krishnamurthy Merlo, Donald J.
                                                                       Conservative
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                                                                   Score 195.6; DB 3;
Pred. No. 2.8e-28;
0; Mismatches 239;
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APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Hadduri, Krishnamurthy
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Sp.
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT APPLICATION NUMBER: US 09/36987
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
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US-09-370-700-1
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                                                                                                                                                          Query Match
Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 80161
TYPE: DNA
ORGANISM: Saccharopolyspora spinosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09370700 Patent No. 6274350
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        39421
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                                                                                                                                                      Score 195.6; DB 3;
Pred. No. 2.8e-28;
0; Mismatches 239;
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Kathryn P
APPLICANT: Maddwri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
FITTE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/603,207B
CURRENT FILING DATE: 2000-06-23
EARLIER APPLICATION NUMBER: 09/370,700
EARLIER APPLICATION NUMBER: 09/370,700
FEARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 80161
TYPE: DNA
GRGANISM: Saccharopolyspora spinosa
US-09-603-207-1
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US-09-603-207-1
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 Query Match
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Matches 361
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ilarity 59.0%;
Conservative
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Score 195.6; DB 3;
Pred. No. 2.8e-28;
0; Mismatches 239;
                                    Length
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                                      80161
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GCCTCCTACGCGGCGGCGACGCCTTCCTCGACGCCTTCGCCCGTCGTCGTCGGCGCAGT 60

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GEN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
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US-08-804-227C-7
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                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: Pebruary 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39541
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NAME/KEY:
LOCATION:
US-08-804-227C-7
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Best Local Similarity 60.1%;
Matches 363; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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                      ACCG
                                                  GCGACCGGACTCGTACTGCCCGCGACGGTCATCTTCGACCACCCCACCGTGGACCGGCTC
                                                                                 GTGACCGGGGTCCGGCCACGACCATCGTCTTCGACCACCGCACAGTGGACCGCCTC
                                                                                                                                       TTCCGTGACCTGGGATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCGGGG
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                                                                                                                                                                                                                                                    CGCGTCGACGCCCTCACCCCGCGCGAGCGCACCAAGGTCCTGGTCGACCTGGTCCGC
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350..14002
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Pred. No. 8.3e-26;
0; Mismatches 226;
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US-08-804-198-1
                                                                                                                                                                               ; LOCATION:
US-08-804-198-1
                                                                                                                     Matches 363;
                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08804198 Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                             FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Richardson, Mark A.
APPLICANT: ROSteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE
                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 44377 base pairs
TYPS: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                            NAMB/KBY:
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                                                        TATGCGGCGATGCGCATCTGGATGCGTTGGCGGAGCGTCGTCGTGCGCAGGGGCGT
CCCGCGACCTCCGTCGCCTGGGGGCCTGTGGGGCGGGCGAGGGGCATGGGAAGCGGAAGGC
                                                                                      TACGCGGCGCAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGTGGGCTG
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LILLY CORPORATE CENTER
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                                                                                                                     Conservative
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Kuhstoss, Stuart A.
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Richardson, Mark
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                                                                                                                   Score 182.4; DB 2;
Pred. No. 8.3e-26;
0; Mismatches 226;
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Patent No. 5876991
                 TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                   ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  COMPUTER: IBM Compatib
OPERATING SYSTEM: MS-D
SOPTWARE: ASCI(DOS) Te:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                               APPLICATION NUMBER: US/08, FILING DATE: February 21, CLASSIFICATION: 435
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MOLECULE TYPE: DNA (genomic) FEATURE:

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

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FEATURE:
NAME/KBY:
LOCATION:
US-08-804-227C-1
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Best Local S
Matches 335
Sequence 32, Application US/09105537A Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
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FEATURE:
NAME/KEY:
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FEATURE:
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                                                                                                                                  GCGGACGGAAGCTGCCGCCGACGCTGTCTTCGACCATCCGACTG 35711
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                                                                                                                                                            CCGGGGTCCGGGTGGCCACGACCATCGTCTTCGACCACCCGACAG
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nilarity 57.3%;
Conservative
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20010..31199
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Pred. No. 5.7e-24;
0; Mismatches 244;
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; APPLICANT: Xue, Y.;
; APPLICANT: Zhao, L.
; TITLE OF INVENTION. DNA encoding methymycin and
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 32
; ELENGTH: 11220
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-32
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Pred. No. 6.8e-24;
0; Mismatches 238;
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RESULT 13
US-09-105-537-5
; Sequence 5, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Liu, H.
; APPLICANT: ARO, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION UMMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
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US-09-320-878-19
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FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
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; TYPE: DNA
; ORGANISM: Streptomyces
US-09-105-537-5
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; SEQ ID NO 5
FENGTH: 36778
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Best Local
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE
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Pred. No. 6.8e-24;
0; Mismatches 238;
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
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Best Local (
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EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
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Local Similarity 57.3%;
hes 340; Conservative
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Pred. No. 6.8e-24;
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RESULT 15
US-09-141-908-1
; Sequence 1, Application US/09141908
; Patent No. 6503741
; Patent No. 6503741
; Patent No. 6503741
; PAPLICANT SETLACH, Gary
; APPLICANT BETLACH, Melanie C.
; APPLICANT BETLACH, Mary
; APPLICANT HODANIEL, Robert
; APPLICANT HODANIEL, Robert
; APPLICANT TANG, Li
; TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced
; TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
; FILE REFERENCE: 300622002100
; CURRENT APPLICATION NUMBER: US/09/141,908
; CURRENT FILING DATE: 1998-08-28
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Using

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EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 31
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
ORGANISM: Streptomyces venezuelae
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Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	Match	Match Length DB	Ħ	ID	Description
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ω	79.2	13.2	1143	S	BU502934	
4	75.6	12.6	888	10	AG030591	
ი 5	75.2	12.5	925	10	CNS0091P	
6	74.8	12.5	935	10	CNS006XK	
7	73	12.2	1169	σ	BQ922913	
с 8	72.8	12.1	852	10	AG060114	AG060114 Pan trog
9	72.8	12.1	985	σ	CA981964	
10	72.6	12.1	1003	10	AG159111	AG159111 Pan trog
c 11	72.2	12.0	1469	10	AG365356	Mus
12	71.8	12.0	1152	10	AG076818	Pan
13	71.6	11.9	996	10	AG072414	Pan
C 14	71.6	11.9	1101	10	AG039543	Pan
c 15	71.6	11.9	1440	10	AG332984	BnW.
16	70.8	11.8	935	10	CNS006XK	AL066051 Drosophi
17	70.4	11.7	492	7	C0851644	CO851644 LM SH5 C
18	70.4	11.7	519	7	C0825295	CO825295 LM GB5 C
19	70.4	11.7	536	7	CO851640	CO851640 LM SH5 00
20	70.4	11.7	581	7	CO834687	
21	70.4	11.7	592	7	C0851643	-
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## ALIGNMENTS

ORIGIN	FEATURES	REFERENCE AUTHORS TITLB JOURNAL COMMENT	RESULT 1 CNS0091P LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Drosophila melanogaster" /mol_type="genomic DNA" /db xref="taxon:7227" /clone="BaCR19D16" /clone_lib="RPCI-98" /note="end : TET3"	melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  1 (bases 1 to 925) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Bp 191 19106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr BP 191 19106 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).	CNS0091P  925 bp  DNA  linear GSS 03-JUN-1999  Drosophila melanogaster genome survey sequence TET3 end of BAC #  BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  AL053013  AL053013  AL053013.1 GI:4934461  GSS.  Drosophila melanogaster (fruit fly)  Drosophila melanogaster (fruit fly)  Drosophila melanogaster (fruit fly)  Drosophila melanogaster

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pacs1-60_6778, genomic survey sequence.
BZ557931
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Fax: 2066857244
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
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Contact: Chris K. Raymond
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                            shotgun
                                                                                                                                                                                                                                                                                                                               craymond@u.washington.edu
                                                                                    /clone="pacs1-60_6778"
/clone_lib="pacs1-60"
/note="clinical isolate
library."
                                                                                                                                                                                               /organism="Pseudomonas
/mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                                                      1. .1438
                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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  13.4%;
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  Score
Pred.
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80.2; DB 9;
No. 3.7e-06;
                                                                                                                                                                                                                                             aeruginosa"
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AGENCOURT 8929661 NIH MGC 94
5', mRNA sequence.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
  found through the I.M.A.G.E. http://image.llnl.gov
                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                       BU502934.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              BU502934
                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
count through the I.M.A.G.E. Consortium/LLNL at:
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                                  Pan troglodytes
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                            AG030591 888
Pan troglodytes DNA, clone: EAG030591
AG030591.1 GI:16557464
 Pujiyama,A.,
                                                                   Pan troglodytes (chimpanzee)
                        Hominidae;
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/lab host="NH108 (phage-resistant)"
/clone lib="NIH MGC 94"
/clone lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: this is a NIH_MGC Library."
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/clone="IMAGE:6489733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                        Pan.
 Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
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                                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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 Toyoda, A.,
                                                                                                                   PTB-003A10.F,
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Taylor, T.D.,
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 CCAGGCCA 546
                       ccaecciegacac - - ccicecetiegerccaeececiceecaeccegarcaaceicec
                                                                                                                                         CCGCCCTGTCCACTGTGGTCTCTCTGCTCGCGCCCGAGGGCGGTGCTGTCGACGACC
                                                                                                                                                               TGTTGTGCACCGCGCAGTCGCGCGCCCGGATCGGCGCACTCGACGCCGTCGACGGCA 360
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Mismatches

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u V

Gaps

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857

478

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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC end sequences of Library Unpublished
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                                                                                                                                                                                                                                                                                                                                        Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing: -21M13
                                                                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-003A10.F"
                                                                                                 /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC
                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
Score 75.6;
Pred. No. 3.
DB 10;
3.2e-05;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr -
Web : www.genoscope.cns.fr -
Web : www.genoscope.cns.fr -
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila BAC clones the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                             52;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AL053013
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                              GETGACCGGAGCGGCAGTACCCCCCGGCCTGGACCGGCCTGGTACGGCCTGGAACA 283
                                                                                           SVVSSASSSSSSSSSVSCSSVASSMSCSSBSSSSASASSSSSSSSASCASCSCCCTSWS
                                                                                                                                                                    GCGCGGGGCGACCGTGTTGTGCACCGCGCAGTCGCGCGCCCGGATCGGCGCGCACT
                                                                                                                                                                                                                                                                                                                     CSCSCSSBSCSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSSSGT
                   CGGTGCTGTCGACGACCCCAGCCTGGACACCCCTCGCGTTGGTCCAGGCGCTCGGCGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
|mol type="genomic DNA"
|db_xref="taxon:7227"
|clone="BACR19D16"
|clone="BACR19D16"
|clone lib="RPCI-98"
|note="end : TET3"
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                             GSCCCSGSCCCSCSCGCCSSCSCSCSSCSCSCSCSCSCGCSCGCSGSSCCSCGCGCSGS
COACCGTCGTGTTGTGCACCGCGCAGTCGCGCGCCCCGGATCGGCGCCGCACTCGACGCCG
                                                                        SEGCGGCSGGCCGSSCCGCSGKSKCGCGCGSGGSCSSSSSGSGSCGGSGGSGCSSCSSGCS
                                                                                                             GAGCGGCAGTACCCCCGGCCTGGACGGACGTGGTCCGCGACGGCCTGGAACAGCGCGGGG
                                                                                                                                                    SSGCGCCCSGGSCGCCCGSCGGSCSCCSSSCCGCGCCGSCSCGCCGGCCGGCSGCCSGGCC
                                                                                                                                                                                     CCTGGCACCCGTCGACCTCGGGGGGTCCTCCCCTGGCCGGACGGGTCCTGGTGGTGACCG
                                                                                                                                                                                                                                                              GGCTCCCGGTCCCCTGGGCCGGGTCCCCGACACCGGCGACGAGTGGCGTTACCAGCTCG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to
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/note="end : T7"
                                                                                                                                                                                                                                                                                                                       12.5%;
                                                                                                                                                                                                                                                                                                     114;
                                                                                                                                                                                                                                                                                                   Score 74.8; DB 10;
Pred. No. 4.6e-05;
4; Mismatches 172;
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Indels

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Gaps

847

231

787

351

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AL066051
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BACR14N09 of RPCI-98 library from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
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                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|db_xref="taxon:7227"
|clone="BACR14N09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA linear GSS 03-JUN-1999
survey sequence T7 end of BAC #
Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D
cccccreeecceeccceacacceceaceaceaceaceacereccreeccaeccreecaecc
                                                                                  GGGACGCCCGGTCGACCTGCCGGTCTACCCCGTTCCAACGACAGAACTTCTGGCTCCCGGT 121
                                                                                                             CGCGCTCGCCGAGGCGTACACCCGGGGGGGGGGGGGAGGTCGACTGGCGTACCGCAGTGGGTGA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1169)
                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 147.
Location/Qualifiers
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:6396111."
/clone="DH10B (T1 phage-resistant)"
/clone=lib="NCI_CGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                                                                                            mol
                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                             strain="FVB/N"
                                                                                                                                                                                     12.2%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                         type="mRNA"
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                                                                                                                                                                                     Score 73; DB 5;
Pred. No. 0.00011;
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                                                                                                                                                                                                 DB 5; Length 1169
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Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pujiyama,A., Hattori,M., Toyo
Totoki,Y., Watanabe,H. and So
BAC end sequences of Library
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AG060114.1 GI:16611344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG060114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   troglodytes (chimpanzee)
                                                                                                                                                                                                    Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                                           Sequencing: -21M13
                                                                                                                                                                                                                                                                                                                                     tracking errors.
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                       /sex="male"
/cell_type="
                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                   organism="Pan troglodytes"
                                                                                                                                                                               ocation/Qualifiers
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                                                                      clone="PTB-047105.F"
                                                                                                                                                               . 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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nd Sakaki, Y.
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                                                                                                                                                                                                                    985 bp
AGENCOURT 11280952 Wellcome CRC
IMAGE:6870527 5', mRNA sequence.
CA981964
CDNA Library Preparation: N. Garrett, P. LeMaire, A J.B. Gurdon (Wellcome/CRC Institute) CDNA Library Arrayed by: The I.M.A.G.B. Consortium DNA Sequencing by: Agencourt Bioscience Corporation
                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: N. Garrett,
Gurdon (Wellcome/CRC Institute)
                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 985)
                                                                                                                                                                           Xenopus laevis (African clawed frog) Xenopus laevis
                                                                                                                                                                                                             CA981964.1 GI:27514618
                                                                           Contact: Robert Strausberg,
                                                                                       Unpublished (1997)
                                                                                                                                                      Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTGGTGGTGACCGGAGCGGCAG
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0; Mismatches 308;
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                                                     P. LeMaire,
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GSS.
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Plate: LLAM14501 row: a column: 22
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/tissue_type="egg"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome_CRC_pSK egg"
/clone_lib="Wellcome_CRC_pSK egg"
/note="Vector: pBluescript_SK-; Site_1: NotI; Site_2:
/note="Vector: pBluescript primed_and_directionally_BCoRI; cDNAs were ollop-dT primed_and_directionally_cloned. Library_was constructed_by N. Garrett, P. LeMair_A.M. Zorn, and J.B. Gurdon (Wellcome/CRC_Institute).
Note: This is a Xenopus Gene_Collection (XGC) library."
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/mol_type="mRNA"
/db_xref="taxon:8355"
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Pred. No. 0.00012;
0; Mismatches 282
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Metazoa; Chordata;

Craniata;

Vertebrata;

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Clones are derived from the chimpanzee BAC library RPCI-43 This BAC Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end was generated during the R&D process and may have higher chance
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R.Site 2
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-024I16.T7"
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Pred. No. 0.00013;
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Best Local (
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                                                             146 CGGCGACGAGTGGCGTTACCAGCTCGGCTCGGCACCTCCGGGCGGTCCTCCCT
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector
R.Site 1
R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ezawa, K.,
Shiroishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing : T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 14 (12), 2439-2447 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence-SNP analysis
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                                                                                                    TACCCG-TTCCAACGACAGAACTTCTGGCTCCCGGTCCCCTGGGCCGGGTCCCCGACAC 145
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus molossinus"
/mol type="genomic DNA"
/sub_species="molossinus"
/db xref="texon:57486"
/clone="MSMg01-168A20.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .1469
                                                                                                                                                                                                                                                                                                                          tissue_type="mixture of kidney and spleen'/clone_Tib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                     sex="male"
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                                                                                                                                                                                                                                            Score 72.2; DB 10; Pred. No. 0.00015;
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes
Bukaryota; Metazoa;
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AG076818
AG076818.1 GI:16628620
GSS.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (chimpanzee)
                                                                                                                                                                                                     clone tracking errors.
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                                                                                                                           Vector
R.Site
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                                                                                                                                                                              Sequencing: M13Rev
                       /sex="male"
/cell_type=
          /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                            /mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                             Location/Qualifiers
                                                 clone="PTB-071C05.R"
                                                                                      organism="Pan troglodytes"
                                                                                                                           r : pKS145
e 1 : SacI
e 2 : SacI.
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Query Match
Best Local Similarity
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Pan troglodytes DNA, clone: E
AG072414
                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); apan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.gp.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes
Pan troglodytes
                                                                                                                               clone tracking errors.
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Sequencing: M13Rev
LIBRARY
                                                                                       PRIMERS
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Pred. No. 0.00018;
0; Mismatches 250;
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PTB-063011.R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor, T.D.,
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genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yada, T.,
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RESULT 14
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AUTHORS
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ORGANISM
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                                                        Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniat;
Mammalia; Eutheria; Euarchontoglires;
                                                                                                                                                  Pan troglodytes DNA, clone: AG039543
AG039543.1 GI:16568268
GSS.
Fujiyama,A.,
                                                                                                                              Pan troglodytes (chimpanzee)
                                             Hominidae;
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R.Site
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/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                          Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="male"
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  Hattori, M.,
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46.9%;
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Pred. No. 0.0002
0; Mismatches 30
                                                                                                                                                                                                                                          1101
Toyoda, A.,
                                                                                                                                                                                                                 1 bp DNA
PTB-016K22.F,
                                                            Craniata; Vertebrata; Euteleostomi; oglires; Primates; Catarrhini;
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Taylor, T.D.,
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Matches 224; Conserv
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Clones are derived from the chimpanzee BAC library PTB This BAC enc was generated during the R&D process and may have higher chance of clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB unpublished
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ilarity 46.4%;
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/clone_lib="PTB Chimpanzee Male
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-016K22.F"
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Pred. No. 0.0002;
0; Mismatches 257;
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Best Local Similarity
Matches 254; Conserv
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Direct Submission

Submitted (17.NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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Shiroishi,
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R.Site
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AG332984 AG332984.1 GI:47906294 GSS.
Mus musculus molossinus (Japanese wild mouse)
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Genome Res. 14 (12), 2439-2447 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e-mail: abe@rtc.riken.jp
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CCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTCGGTGGTGGTTGACCGGAGCGGCAG
                                                            TCCCCTGGGCCGGGTCCCCGACACCGCGACGAGTGGCGTTACCAGCTCGCCTGGCACC
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                                                                                                                                                                                                                                                                                 11.9%;
ilarity 47.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="rtaxon:57486"
/clone="MSNG01-123F20.T7"
/sex="male"
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/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                   Score 71.6; DB 1
Pred. No. 0.0002;
0; Mismatches 28
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Search completed: April 7, 2006, 14:04:00 Job time : 2314.57 secs

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Minimum DB
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3: geneseqn2000
                   9:
10:
11:
12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
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601
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Listing first 45 summaries
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11689.676 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Length	80	ID	Description
_	601	100.0	17596	12	ADI14148	Adil4148 M. megalo
N	601	100.0	47981	4	AAF30757	Aaf30757 Micromono
w	397.8	66.2	29879	N	AAQ46806	Aaq46806 eryA reqi
4	281	46.8	9510	12	ADM97245	Adm97245 Syntheti
ហ	220.2	36.6	4725	10	AAD55818	Aad55818 Micromono
6	220.2	36.6	60196	10	AAD55810	
7	207.6	34.5	9684	13	ADQ91711	1
œ	207.6	34.5	9684	L3	AEB87003	ω
9	207.6	34.5	9684	13	AEB86800	0
10	207.6	34.5	164051	13	ADQ91695	•
11	207.6	34.5	164051	13	AEB86862	
12	207.6	34.5	164051	13	AEB86659	-
13	204.4	34.0	5355	10	AAD55819	Aad55819 Micromono
14	201.6	33.5	67167	14	ADY80053	Ady80053 Nucleotid
15	200.6	33.4	104096	13	ADX56092	
16	199	33.1	24444	13	ADQ91699	Adq91699 Polyketid
17	199	33.1	24444	13	AEB86991	
18	199	33.1	24444	13	AEB86788	
19	198.8	33.1	113193	00	AAD54645	Aad54645 Streptomy

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44	ι 43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20
172.2	172.2	172.2	172.2	172.6	173.2	174	174	180.2	182.4	182.4	182.8	182.8	182.8	184.2	184.2	185.2	186	190.6	193.4	193.4	195.6	195.6	195.6	195.6
28.7	28.7	28.7	28.7	28.7	28.8	29.0	29.0	30.0	30.3	30.3	30.4	30.4	30.4					31.7	32.2	32.2	32.5	32.5	32.5	32.5
36778 37948	36778	11220	11220	43280	15872	82746	4770	14775	44377	44377	4974	4974	4974	125401	27541	138203	75236	74787	73599	9795	80161	50000	50000	9513
3 12	ω	12	ω	N	N	œ	œ	4	N	N	13	13	13	4.	4,	14	10	12	14	14	N	4	4.	4
ADL91933 AAZ87285	AAZ87318	ADL91917	AAZ87298	AAT80413	AAT68715	AAL61224	AAL61172	AAF88338	AAT78508	AAT80414	AEB86794	AEB86997	ADQ91705	AAD17186	AAD17185	ADZ51725	ABV75557	ADQ74672	ADY72575	ADY72595	AAZ21501	AAF88316	AAF88313	AAF88337
Ad191933 Streptomy Aaz87285 S. venezu	Aaz87318 S. venezu	Adl91917 Streptomy					Aal61172 Actinosyn	Aaf88338 S. spinos	Aat78508 Platenoli	Aat80414 Platenoli	Aeb86794 Streptomy	Aeb86997 Streptomy	Adq91705 Polyketid	Aad17186 Streptomy	Aad17185 Streptomy				P01	Ady72595 A. orient	Aaz21501 DNA fragm		Aaf88313 S. spinos	Aaf88337 S. spinos

## ALIGNMENTS

ADI14148 standard; DNA; 17596 BP

ADI14148;

15-APR-2004 (first entry)

M. megalomicea cosmid KOS205-57-2.3B SEQ ID NO:2.

ds; polyketide; enzyme; MegR; MegR; MegK; MegCIV; MegBVI; MegBIII; MegL; MegM; megOsamine; megalomicin.

Micromonospora megalomicea.

WO2004003169-A2.

08-JAN-2004.

30-JUN-2003; 2003WO-US020681

28-JUN-2002; 2002US-0393016P

(KOSA-) KOSAN BIOSCIENCES INC.

Hutchinson RC, Katz L, Reid R, 품 Ņ, Gramajo H;

WPI; 2004-203379/19.

Novel isolated, purified, or recombinant nucleic acid comprising polyketide modifying gene, there gene encodes polyketide modifying enzyme e.g., MegR, MegK, or MegM enzymes useful for producing modified

Example 2; SEQ ID NO 2; 51pp; English.

RESULT 1
ADII14148
ID II 14148
ID II 4148
ID II 524
AC ADII1
XX MegL
XX MegL
XX MegL
XX ADII1
XX ADIII
XX ADIII
XX ADII1
XX ADII1
XX ADII1
XX ADII1
XX ADII1 The invention relates to a novel isolated, purified, or recombinant nucleic acid (1) comprising a polyketide modifying gene, where the gene encodes a polyketide modifying encodes a polyketide modifying encodes near Megr, Megr, Megk, Megk, Megk, Megk, MegCIV, MegCV, MegCV, MegGVIV, MegGVIV,

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RESULT 2
AAR30757
ID AAR30757
ID AAR3
XX AAR3
XX AAR3
XX AAR3
XX AAR3
XX Wicr
XX Wicr
XX Mega
XX Micr
XX Anticx
XX Mega
XX Anticx
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Best Local Simi
Matches 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              under conditions in which the cell expresses a product of a gene encoded by the nucleic acid under conditions in which the unmodified polyketide by the nucleic acid under conditions in which the unmodified polyketide is present, and producing the modified polyketide. The cell produces megosamine and can attach megosamine to a polyketide, where the cell, it its naturally occurring non-recombinant state cannot produce megosamine. The present sequence contains downstream megalomicin modification enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                            AAF30757 standard;
Micromonospora megalomicea subsp.
                                                        Micromonospora
                                                                                21-JUN-2001
                                                                                                       AAF30757;
                      antiparasitic;
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Local Similarity
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ilarity 100.0%;
Conservative
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                                                       megalomicea megalomicin biosynthetic
                                 gene;
                                                                                                                            DNA;
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                                                                               entry)
                                 polyketide
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Pred. No. 1.8e-91;
Mismatches 0;
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                                    antibiotic;
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                                    motilide;
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          misc_feature
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/function=
13849. .151
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/*tag= a
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deoxyglucose-"
/note= "encodes AAB82201"
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complement(9226. .10479)
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5822. .6595
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/product= "TDP-4-keto-6-deoxyhexose 4-ketoreductase"
/product= "eryVIV, dumV homolgoue; encodes AAB82208"
complement(8228. .9220)
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/product= "daunosaminyl-N,
/note= "eryCVI homologue;
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/genc= "megy"
/product= "mycarose O-acyltransferase"
/product= "encodes AAB82204"
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/note= "polyketide synthase; encodes AAB82212"
12505. .13470
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"megA"
'``` AT-L"
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                                    "megA"
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              .15126
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                         "ACP-L"
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                                                                                                                                                                                                                                                                                                                                                                                                             encodes AAB82207"
                                                                                                                                                                                          4-ketoreductase"
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/function= "ACP5"
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                                                                                                                                /gene= "megAII"
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/function= "KS1"
15427. .16476
                                                                                                    /*tag= ak
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/function= "KR5"
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         /gene= "megAII"
/function= "KS4"
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/function= "AT5"
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/function= "KS3"
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                                                                                                                                                                                                                                                                                                                                                                                           /gene= "megA"
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                                                                                                                                                                                              24544.
                                                                                                                                                                                                                             24544.
                                                                                                                                                                                                                                                                                          /note= "polyketide
22957. .24237
                                                                                                                                                                                                                                                                                           /gene= "megAII"
/groduct= "megalomicin 6-deoxyerythronolide B synthase
/product= "molvketide synthase, encodes AAB82213"
                                                                             gene= "megAII"
/function= "ACP3"
                                                                                                                                                                                                     gene= "megAII"
function= "AT3"
                                                                                                                                                                                                                                     gene= "megAIII"
function= "KS5"
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function= "ACP2"
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/function= "KR2"
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function= "KS2"
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function= "KR1"
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                      GETGGGGTCCGCCCGGGGCCGAGGAGACCGGTCAGGAATCGGATCTCGCCCGGCGGCTG
                                                     GAGGGCGGCGACTACCTGCGCAGCCAGGGCCTGCGCGCCATGGACCCGCAGCGGGCGATC
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/gene= "megAII"
/function= "KR4"
32257. .32799
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/function= "KS6"
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/function= "KR6"
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/function=
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function= "TB"
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function= "ER4"
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function= "AT4"
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:ion= "AT6"
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25-MAR-2003
22-DEC-1993
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This sequence represents a fragment of the Saccarapolyspora erythraea genome, designated eryA. The polypeptides encoded by this region are involved in the biosynthesis of the polyketide segment of erythromycin eryA is organised in modules and each module takes care of one condensation step. The precise succession of elongation steps is dictated.
                                                                                                                                                                                           Biosynthesis of specific polyketide analogues esp. erythromycin cpds. - by introducing altered biosynthetic gene-contg. DNA into microorganisms.
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ation; acyl chain growth;
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CTGGGATTCGACTCCATGACCGCCGTCGACCTGCGGAACCGGCTCGCGGCGGTGACCGGG
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                                                     The invention relates to genes and proteins involved in the biosynthesis of macrolides by microorganisms. In particular it relates to the nucleic acids forming the biosynthetic locus for rosaramicin (a 16-member macrolide antibiotic) from Micromnospora carbonacea. The invention is useful for the biosynthesis of macrolides by microorganisms. It allows direct manipulation of macrolides and related chemical structures by chemical engineering of the proteins involved in the biosynthesis of rosaramicin. It is useful to catalyse certain biochemical reactions, in vitro or in vivo, to direct or enhance the synthesis or modification of spolyketide, polyketide substrate or its precursor. The present sequence is M. carbonacea polyketide synthase (PKS) type I gene. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptide involved in biosynthesis of macrolides by microorganisms, useful for biosynthesis of macrolides by microorganisms, preferably for biosynthesis of rosaramicin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 164-166; 206pp; English.
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07-AUG-2003
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                                                                                                                        Micromonospora
                                                                                                                                           gene;
                                                                                                                                                                      Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster
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                                                                                                                                                   rosaramicin; polyketide; polyketide synthase; PKS; enzyme;
                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                          carbonacea
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/product= "Polyketide synthase
complement(2629. .3861)
                                             complement (1728. .2522)
                                                                                                    Location/Qualifiers
                                                       partial/
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/note= "CDS does not include start codon"
product= "Polyketide synthase #3"
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                                     ECOPIA BIOSCIENCES INC
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/*tag= d

/product= "Polyketide 8

5702. .19117
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57657..59123
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/note= "CDS does not include start
/partial
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54897, .56342
                                                                                                                                                                                                                                                                                        complement (54569. .53358)
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/product= "Polyketide synthase #14"
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19092. .49814
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'product= "Polyketide synthase #13"
/transl except= (pos:51221. .51223, aa:Xaa)
/note= "Xaa corresponds to amino acids from
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Matches 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide involved in biosynthesis of macrolides by microorganisms, useful for biosynthesis of macrolides by microorganisms, preferably for biosynthesis of rosaramicin.
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C 40770
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                                                                                                                                                                                                          GATCGGATTCGACTCGCTGACCGCCGTCGACCTGGCCAAGCGGCTCAGGGCGGCGGCGGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCCTCCTGGCCGCCCTGGACCGGGACGACGTCGTCGTCGCCGACGTGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGCTGCGGACCACCCTGGACGCCGGGGACCCGTGGGTGCTCGGTGGACCTGGACCG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60196 BP; 6934 A; 20042 C; 23822 G; 9398
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61.6%;
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Pred. No. 3.4e-28;
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RESULT 7
ADQ91711
ID ADQ
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Best Local Similarity
Matches 376; Conserv
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13-MAY-2003;
01-AUG-2003;
13-AUG-2003;
                                                                                                                                                                                                                                                                                           The present invention relates to novel Streptomyces aizunensis (NRI 11277) polyketide synthases and their coding sequences for polyene polyketide production. The polyketides are useful as fungal growth inhibitors and cancer cell growth inhibitors. The present sequence coding sequence for a polyketide synthase of the invention.
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                            Isolated, purified or enriched nucleic acid useful for producing polyketides, encodes domains of the polyketide synthase system.
                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bachmann
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polyketide;
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                                     GAGGAGCTGCGGACCCTGGACGCCGGGGGACCCCGTGGGTGTCGGTGGTGGACCTGGAC
                                                                                                                      GGACTGCCCGCCACCTCCATCGCCTGGGGCCCTTGGGGGCGACGGGGGCATGGCCGAGGGC
                                                                                                                                             GGGCTGCCGGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGGCAGAACATGGCCGGTACC 120
                                                                                                                                                                     GGCAACTACGCGCGGGCAACGCGTTCCTGGACGCCTTCGCCGAGTACCGCCGGGCATCC 4113
                                                                                                                                                                                             GCTCCTACGCGGGGGAACGCCTTCCTCGACGCCTTCGCCGTCGTGGTCGCGCGAGT
                                                                                                                                                                                                                                                                     9684 BP; 1211 A; 3372 C; 3596 G; 1505 T;
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                       GCCGCACTCCAGCACGCCCTGGACCGCGACGACGACCCTGACCGTCGCCGACATGGAG
                                                                      GCGGTCGGTGACCGGATGCGCCACGGGGTCATCGAGATGTCGCCCGAGCGTGCCGTC
                                                                                            GAGGGCGACTACCTGCGCAGCCAGGGCCTGCGCGCCATGGACCCGCAGCGGGGATC
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 34; 554pp; English.
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; 2003US-0469810P.
; 2003US-0491516P.
; 2003US-0494568P.
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Pred. No. 5.2e-26;
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13-MAY-2003;
01-AUG-2003;
13-AUG-2003;
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gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces aizunensis polyketide synthase ORF16 DNA SEQ ID NO:34.
  The invention relates to an isolated, purified or enriched nucleic acid which can be used for the production of a polyketide. The nucleic acid
                                                                                                       Isolated, purified or enriched nucleic acid useful polyketides, encodes domains of the polyketide synt
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                                                               Claim 2; SEQ ID NO 34; 550pp; English
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; 2003US-0469810P.
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CC encodes at least one domain of the polyketide synthase system formed by CC the polyketide synthases of AEB86865, AEB86867, AEB86871, AEB86873, AEB86873, AEB86877, AEB86877, AEB86873, AEB86874, AEB86874, AEB86876, CC an isolated, purified or enriched nucleic acid selected from the group CC consisting of AEB86866, AEB868676, AEB86874, AEB86876, CC AEB86878, AEB86880 and AEB86882; (2) an isolated, purified or enriched cc nucleic acid for the production of a polyhetide; (3) an CC expression vector comprising the novel nucleic acid or the nucleic acid cor the commid deposited under IDAC accession no. 250203-01, 250203-02, CC 250203-03, 250203-04, and 250203-05; and (6) an isolated polypeptide for the production of a polyketide. The nucleic acid can be used for production of a polyketide, for use as a fungal and cancer cell growth conhibitors. The present sequence encodes Streptomyces aizunensis polyene conhibitors. The present sequence encodes Streptomyces aizunensis polyene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                    AACCGGCTCGCGGCGGTGACCGGGGTCCGGGTGGCCACGACCATCGTCTTCGACCACCCG
                                                                                                                                     GAGGCGGGCCTTCAAGGAGCTGGGCTTCGACT
                                                                                                                                                                 GAGCGTGACGTCGCCTTCCGTGACCTGGGATTCGACTCCATGACCGCCGTCGACCTGCGG
                                                                                                                                                                                                                            CTCGAACTGGTCCGCCGTCGCCGTCGCCGTCCTCGGCTACGCGGGCCCCGACGCGGTC
                                                                                                                                                                                                                                                                      GCCCGGCTGGTCCGAGCCGAGGTGGCAGCGGTGCTGGGCCACGGCACGCCGACGGTGATC
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ACAGTGGACCGCCTCACCGCGCAC
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60.3%;
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Pred. No. 5.2e-26;
0; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- CGCCGGGGCCGAGGAGACCGGTCAG
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standard; DNA; 9684

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                                                                                                                                                                                                                               The invention relates to an isolated, purified or enriched nucleic acid condess at least one domain of the polyketide. The nucleic acid condess at least one domain of the polyketide synthase system formed by the polyketide synthases of AEB86662, AEB86664, AEB86668, AEB86668, Condessating of the polyketide synthases of AEB86662, AEB86668, AEB86668, AEB86669, AEB86672, AEB86672, AEB86678, AEB86669, AEB86678, AEB86678, AEB86678, AEB86678, AEB86678, AEB86678, AEB86679, AEB86679, AEB86673, AEB866
                                                                                                                           Query Match
Best Local Sim
Matches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2003;
13-MAY-2003;
01-AUG-2003;
13-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyene polyketide compounds are bacterial cell for treating e.g. fungal infections and cancer.
                                                                                                                                                                                         Sequence 9684 BP; 1211 A; 3372 C; 3596 G; 1505 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Farnet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyene; polyketide; polyketide synthase; antifungal; cytostatic; cancer;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ECOP-)
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                                                                                                                                            Similarity
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                                                                                                                                                                                                                            invention
GGACTGCCCGCCACCTCCATCGCCTGGGGCCCTTGGGGCGACGGGGGCATGGCCGAGGGC
                              GGGCTGCCGGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGGCAGAACATGGCCGGTACC
                                                                              GCCTCCTACGCGGCGAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2003US-0441123P.
; 2003US-0469810P.
; 2003US-0491516P.
; 2003US-0494568P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bachmann
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                                                                                                                                        34.5%;
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0; Mismatches
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Pred. No. 5.
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5.2e-26;
hes 224;
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RESULT 10
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                                                   /product= "Polyketide
61852. 77475
             /product= "Polyketide synthase
77606. .93904
                                                                                                                                                                                 /product= "Polyketide
25902. .36188
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1375. .25818
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36213. .56468
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P-PSDB; ADQ91696; ADQ91698, ADQ91700, ADQ91702, ADQ91704, ADQ91706, ADQ91708, ADQ91710, ADQ91712, ADQ91714, ADQ91716, ADQ91718, ADQ91720, ADQ91724, ADQ91724, ADQ91724, ADQ91726, ADQ91726, ADQ91726, ADQ91732, ADQ91734, ADQ91736, ADQ91738, ADQ91736, ADQ91738, ADQ91740, ADQ91742, ADQ91744, ADQ91746, ADQ91748, ADQ91750, ADQ91752, ADQ91754.
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present invention relates to novel Streptomyces aizunensis (NRRL B-77) polyketide synthases and their coding sequences for polyene yketide production. The polyketides are useful as fungal growth ibitors and cancer cell growth inhibitors. The present sequence is a contig which comprises thirty Open Reading Frames (ORFs), encoding yketide synthases and related proteins. 21253 A; 59641 C; 58859 ဝ 24298 T; 0 Ç, 0 Other, 9

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RESULT 11
AEB86662
AD AEB86
AC AEB8
AC AEBA
AC AEB8
AC AEB8
AC AE
                                                                                                                                                                                                          The invention relates to an isolated, purified or enriched nucleic acid which can be used for the production of a polyketide. The nucleic acid concodes at least one domain of the polyketide synthase system formed by the polyketide synthases of AEB86867, AEB86867, AEB86871, AEB86871, AEB86871, AEB86873, AEB86874, AEB86874, AEB86874, AEB86874, AEB86874, AEB86874, AEB86876, AEB86870, AEB86872, AEB86874, AEB86876, AEB86876, AEB86870, AEB86872, AEB86874, AEB86876, AEB86870, AEB86873, AEB86876, AEB86876, AEB86870, AEB86872, AEB86874, AEB86876, AEB86876, AEB86882; (2) an isolated, purified acid concilic acid concilicated polypeptide for the committed under IDAC accession no. 250203-01, 250203-02, AEB86876, AEB86876, AEB86882; (3) an isolated polypeptide for the production of a polyketide, for use as a fungal and cancer cell growth conhibitors. The present sequence represents a Streptomyces aizunensis colypens polyketide synthase related contil 2 DNA sequence, which is used in the accentification of the production of the production of a polyketide synthase related contil 2 DNA sequence, which is used in the accentification of the production of the polyketide synthase related contil 2 DNA sequence, which is used in the accentification of the production of the polyketide synthase related contil polyketide.
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13-MAY-2003; 2003US-0469BL0P.
01-AUG-2003; 2003US-04941516P.
13-AUG-2003; 2003US-0494568P.
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Bachmann

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The invention relates to an isolated, purified or enriched nucleic acid which can be used for the production of a polyketide. The nucleic acid encodes at least one domain of the polyketide synthase system formed by the polyketide synthases of AEB8662, AEB8664, AEB86666, AEB86668, an isolated, purified or enriched nucleic acid for the production of a polyketide of Formula I comprising a nucleic acid selected from the group consisting of AEB8663, AEB86665, AEB86667, AEB86673, AEB8667
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Pred. No. 3.7e-26;
0; Mismatches 224
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                                                         Query Match
Best Local Similarity
Matches 359; Conserv
                                                                                                                                           of macrolides by microorganisms. In particular it relates to the nucleic acids forming the biosynthetic locus for rosaramicin (a 16-member macrolide antibiotic) from Micromonospora carbonacea. The invention is useful for the biosynthesis of macrolides by microorganisms. It allows direct manipulation of macrolides and related chemical structures by chemical engineering of the proteins involved in the biosynthesis of rosaramicin. It is useful to catalyse certain biochemical reactions, in tire or in vivo, to direct or enhance the synthesis or modification of polyketide, polyketide substrate or its precursor. The present sequence is M. carbonacea polyketide synthase (PKS) type I gene. (Updated on 27-corr-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide involved in biosynthesis of macrolides microorganisms, useful for biosynthesis of macrolides by microorgy preferably for biosynthesis of rosaramicin.
                                                                                                                 Sequence 5355
                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 176-176; 206pp; English.
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by microorganisms. In particular it relates to the nucleic
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                                                 New isolated, purified, or recombinant DNA molecule encoding a domain or activity of an enzyme required of leptomycin, useful for producing polyketides and
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15-MAR-2004; 2004US-0553384P.
08-SEP-2004; 52US-00553384.
                   Disclosure;
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Pred. No. 4.1e-25;
0; Mismatches 239
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Location/Qualifiers

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The present invention relates to a novel nanoligomycin biological synthetic gene cluster, belonging to the field of gene technology. whole nanoligomycin biological synthetic gene cluster has 13 genes including polyketone synthase genes (7 genes of nlm A1, nlmA2, nlmA)
                                                                WPI; 2004-797302/79.
P-PSDB; ADX56093, ADX56094, ADX56095, ADX56096, ADX56099, ADX56100, ADX56101, ADX56102, ADX56103,
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/note= "This sequence
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/note= "No start c
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Matches 348
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Search completed: April 7, 2006, 03:16:48
Job time: 343.651 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Published Applications NA New:*

1: /SIDS5/ptodata/2/pubpna/USO8 NEW_PUB.seq:*

2: /SIDS5/ptodata/2/pubpna/USO8 NEW_PUB.seq:*

3: /SIDS5/ptodata/2/pubpna/USO7 NEW_PUB.seq:*

4: /SIDS5/ptodata/2/pubpna/USO7 NEW_PUB.seq:*

5: /SIDS5/ptodata/2/pubpna/USO9 NEW_PUB.seq:*

6: /SIDS5/ptodata/2/pubpna/USO9 NEW_PUB.seq:*

7: /SIDS5/ptodata/2/pubpna/USO1 NEW_PUB.seq:*

8: /SIDS5/ptodata/2/pubpna/USIO NEW_PUB.seq:*

9: /SIDS5/ptodata/2/pubpna/USIO NEW_PUB.seq:*

10: /SIDS5/ptodata/2/pubpna/USIO NEW_PUB.seq:*

11: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

12: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

13: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

14: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

15: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

16: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

17: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

18: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

19: /SIDS5/ptodata/2/pubpna/USI1_NEW_PUB.seq:*
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10613.880 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

13 14 15 17 18	10 c 12	0 8 7 6 5 4	c :	Result No.
58.2 58.2 58.2 58.2 57.8	59.4 58.6	63 62 60.4 59.8	78.4 71.2 67.2	Score
9.7 9.7 9.7 9.6	9.9 9.9	10.5 10.3 10.2 10.1	13.1 11.9 11.2	Query Match
984 4470 5679 78869 897 1687	1632 1685 4146	2724 5706 1450 88421 1328 2514	116856 1290 5706	Query Match Length
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Sequence 45, Appl Sequence 44, Appl Sequence 36, Appli Sequence 1, Appli Sequence 45, Appl Sequence 13382, A	Sequence 546, App Sequence 8, Appli Sequence 522, App	Sequence 359, App Sequence 519, App Sequence 12512, A Sequence 1, Appli Sequence 8975, App Sequence 543, App	Sequence 1, Appli Sequence 47, Appl Sequence 519, App	Description

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Sequence 10	Sequence 38	Sequence 22319,	Sequence 1	Sequence !	Sequence 1	Sequence (		Sequence !		Sequence :			Sequence :	Sequence :			Sequence :	Sequence (			Sequence :	Sequence :	Sequence !	Sequence :	Sequence :	neduction.
183, App	38, Appl	22319, A	1205726,	592317,	17168, A	67, Appl	23776, A	543, App	22989, A	21827, A	530, App	24044, A	22600, A	533, App	550, App	24552, A	25313, A	68, Appl	538, App	16581, A	253, App	2, Appli	521, App	23918, A	1690, Ap	Ades to an

### ALIGNMENTS

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APPLICANT: Sulmwate, ....

APPLICANT: Kulowski, Kerry

APPLICANT: Pong, Kevin

FITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex

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US-11-143-980-1
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APPLICANT: Hucul, John
APPLICANT: Haltli, Bradley A.
APPLICANT: Wagenaar, Melissa M.
APPLICANT: Graziani, Edmund
APPLICANT: Graziani, Mia
                                                                                                                                                                                                                                                                                                                                                                                       Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                          Match 13.1%;
Local Similarity 55.0%;
51167
                                                       61 AGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGAACAGAACTTCTGGCTCCCGG 120
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Pred. No. 9e-09;
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; ORGANISM: Streptomyces coelicolor
US-10-858-730-47
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Best Local Similarity 51.9%;
Matches 160; Conservative
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LENGTH: 1290
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APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
APPLICANT: Driggers, Edward |
APPLICANT: Madden, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yorgey, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FASTSEQ for Windows Version 4
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CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
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Madden, Kevin T.
O'Leary, Jessica
O'Toole, George
Trueheart, Joshua
Walbridge, Michael J.
Yorgey, Peter S.
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Pred. No. 8.6e-07;
0; Mismatches 148;
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RESULT 4
US-10-517-939-359
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US-11-052-554A-519/c
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LENGTH: 5706
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis H37Rv
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Sequence 359, Application US/10517939 Publication No. US20060003433A1 GENERAL INFORMATION:
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
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PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
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Local Similarity 47.0%;
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Pred. No. 4.6e-06;
0; Mismatches 233;
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APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geof
APPLICANT: Wu, Di
APPLICANT: Blum, David

Walter

Hazlewood, Geoff Wu, Di Blum, David

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CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR PPLICATION NUMBER: 60/389,299
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 359
LENGTH: 2724
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US-11-052-554A-519
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GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.5%;
Best Local Similarity 45.5%;
Matches 265; Conservative
                                                                              Sequence 519, Appropriate Publication No.
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TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING
FILE REFERENCE: 564462007901
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ORGANISM: Unknown
FEATURE:
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                                                                            Application US/11052554A o. US20050288866A1
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Pred. No. 4.4e-05;
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GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fr.
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12512
LENGTH: 1450
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US-11-096-568A-12512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12512, Application US/11096568A Publication No. US20060048240A1
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SOFTWARE: PatentIn versio
SEQ ID NO 519
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                         PEATURE:
NAME/KRY: misc feature
LOCATION: (1). [1450)
OTHER INFORMATION: Ceres Seq.
                                                                                                                                                                  TYPE: DNA ORGANISM: Triticum aestivum
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Pred. No. 6.3e-05;
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Query Match 10.2%;
Best Local Similarity 45.0%;
Matches 229; Conservative
Score 61; DB 11;
Pred. No. 0.00014;
0; Mismatches 280;
                            Length 1450;
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PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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Publication No. US20050287641A1
GENERAL INFORMATION:
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APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
FILE REFERENCE: 3002-2US
CURRENT APPLICATION NUMBER: US/11/205,109
CURRENT FILING DATE: 2005-08-17
PRIOR APPLICATION NUMBER: US/09/976,059
PRIOR FILING DATE: 2001-10-15
              FEATURE:
NAME/KEY: misc_feature
LOCATION: (4038)..(504)
OTHER INFORMATION: ORF
                                                                                   FEATURE:
NAME/KEY: misc feature
LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2
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LOCATION: (2077)..(3078)
OTHER INFORMATION: ORF 1;
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FEATURE:
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FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
(7703)..(669
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NAME/KEY: misc_feature
LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8;
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LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10;
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LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4
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LOCATION: (15591)..(15863)
OTHER INFORMATION: ORF 11;
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LOCATION: (9464)..(8130)
OTHER INFORMATION: ORF 6
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NAME/KEY: misc feature
LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17;
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LOCATION: (66546)..(67370)
OTHER INFORMATION: ORF 16;
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LOCATION: (65826)..(66530)
OTHER INFORMATION: ORF 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (39713)..(65800)
OTHER INFORMATION: ORF 14;
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LOCATION: (19032)..(39713)
OTHER INFORMATION: ORF 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (15880)..(190 OTHER INFORMATION: ORF
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NAME/KEY: misc feature
LOCATION: (13617)...(12802)
OTHER INFORMATION: ORF 9;
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OTHER INFORMATION: ORF 5
                                       NAME/KEY: misc_feature
LOCATION: (74216)..(731
OTHER INFORMATION: ORF
FEATURE:
                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (73439)..(71964)
OTHER INFORMATION: ORF 20;
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19;
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NAME/KEY: misc_feature
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ORF 12;
                                                                   (73563)
ORF 21;
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; NAME/KEY: misc feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORP 33;
US-11-205-109-1
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Best Local &
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LOCATION: (82346)..(82062)
OTHER INFORMATION: ORF 28;
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LOCATION: (87372)..(86803)
OTHER INFORMATION: ORF 32;
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LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31;
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LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29;
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LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27;
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LOCATION: (81674):.(79861)
OTHER INFORMATION: ORF 26;
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LOCATION: (84481)..(85548)
OTHER INFORMATION: ORF 30;
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LOCATION: (78110)..(76449)
OTHER INFORMATION: ORF 24;
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LOCATION: (75535)..(76464)
OTHER INFORMATION: ORF 23;
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OTHER INFORMATION: ORF 22; negative
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Similarity 49.1%;
 GACCAGGGACGCCGCCGCCGTGACCG 516
                             CACCCGCCCGGAGTTCGACGTGCCCGGCATGACGTCGAACGTGGTGCCGCGCGCCCCCGC 16775
                                                         CACCCTCGCGTTGGTCCAGGCGCTCGGCGCAGCCGGGATCGACGTCCCCCTGTGGCTGGT
                                                                                     GGGGGCGCGGCGGACCAGCGTGCCAGGCCAGGCCATCGCGGCCGCCGCCCTCTA
                                                                                                                                                                               CGCGCAGTCGCGCGCGCGCATCGGCGCCCCCACTCGACGCCGTCGACGGCACCGCCCTGTC
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Pred. No. 7.8e-05;
0; Mismatches 166
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RESULT 8
US-11-096-568A-8975
; Sequence 8975, App;
; Publication No. US:
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CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8975
LENGTH: 1328
                                                                                                                                                                                                                                                                                                                                                                       Sequence 543, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA
TITLE OF INVENTION: Therby
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Best Local Similarity
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
                                                                                                                                                                                                                                     APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
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LOCATION: (1)..(1328)
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Pred. No. 0.00021;
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NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
SEQ ID NO 543
LENGTH: 2514
TYPE: DNA
ORGANISM: Mycobactérium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 546, Application US/11052554A Publication No. US20050288866A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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LENGTH: 1632
                                                                                                                                       Matches 180;
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL FILE REFERENCE: 30853/40359A CURRENT APPLICATION NUMBER: US/11/052,554A CURRENT FILING DATE: 2005-02-07
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/589,227 PRIOR FILING DATE: 2004-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sachdeva,
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mycobacterium tuberculosis H37Rv
                                                                                                                                                  Match 9.9%;
Local Similarity 49.6%;
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                                             TCCGCGACGGCTTGGAACAGCGCGGGGGGGGCGACCGTCGTGTTGTGCACCGCGCAGTCGCGCG
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Pred. No. 0.00022;
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Pred. No. 0.0003;
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; TYPE: DNA
; ORGANISM: Saccharopolyspora erythraea
US-11-254-686-8
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SEQ ID NO 8
LENGTH: 1685
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Best Local Similarity 47.0%;
Matches 254; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/11254686 Publication No. US20060040877A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Waldron, Clive TITLE OF INVENTION: Novel Spinosyn-Producing Polyketide Synthases FILE REFERENCE: 62069 CURRENT APPLICATION NUMBER: US/11/254,686 CURRENT FILING DATE: 2005-10-20
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APPLICANT: Burns, Lesley
APPLICANT: Graupner, Paul
APPLICANT: Lewer, Paul
APPLICANT: Vousden, Willi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/358075
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 26
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CTGGCCGCCCAGGCGTTCACCGGCGCGTCGACTGGACCGGCCGCCTACGAC
                                              TTGTGCACCGCGCAGTCGCGCCCCGGATCGGCGCCGCACTCG---ACGCCGTCGACGGC 359
                                                                                               CCCCGGCCTGGACGGACGTGGTCCGCGACGGCCTGGAACAGCGCGGGGGCGACCGTCGTG
                                                                                                                                                                                                                                                                                                 Vousden, William A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59.4; DB 11;
Pred. No. 0.0003;
0; Mismatches 281;
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CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-02-06
PRIOR PILING DATE: 2004-02-06
PRIOR PILING DATE: 2004-03
SOFTWARE: Patentin version 3.3
SEQ ID NO 522
ENOTH: 4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA ; ORGANISM: Mycobacterium tuberculosis H37Rv US-11-052-554A-522
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US-11-052-554A-522/c
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Best Local Sim
Matches 224;
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publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMEUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
1689
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CGGGCCGCCGGCCGGCCCGCCCGCCGGCCGGCCCGCCCGCCGCCGCCGCCGCCGCCTCCCCCGCC
                                                    CTGTGGCTGACCAGGGACGCCGCCGCCGTGACCGTCGGAGACGACGTCGATCCGGCC
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Pred. No. 0.00037;
0; Mismatches 254;
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US-11-228-659-45
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CURRENT APPLICATION NUMBER: US/11/228,65

CURRENT FILING DATE: 2005-09-16

PRIOR APPLICATION NUMBER: 60/610,656

PRIOR FILING DATE: 2004-09-17

PRIOR APPLICATION NUMBER: 60/637,230

PRIOR FILING DATE: 2004-12-17

PRIOR APPLICATION NUMBER: 60/696,405

PRIOR FILING DATE: 2005-07-01
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Best Local Similarity 47.0%;
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Publication No. US20060064786A1
GENERAL INFORMATION:
APPLICANT: Brugiere, Norbert
TITLE OF INVENTION: Isopentenyl Tran
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: OSIPT2
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LOCATION: (1)...(984)
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GATGCACGGCTACCTGCTGGCGGAGCGCGAGGGCGCCGGCGCCGACGACGACGACGA
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Pred. No. 0.00061;
0; Mismatches 238;
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FILE REFERENCE: 1507

CURRENT APPLICATION NUMBER: US/11/228,659

CURRENT FILING DATE: 2005-09-16

PRIOR APPLICATION NUMBER: 60/610,656

PRIOR APPLICATION NUMBER: 60/637,230

PRIOR APPLICATION NUMBER: 60/696,405

PRIOR PILING DATE: 2005-07-01

NUMBER OF SEQ ID NOS: 87

SOPTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 44

LENGTH: 4470
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US-11-228-659-44
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APPLICANT: Bruglere, Norbert
TITLE OF INVENTION: Isopentenyl Transferase Sequences
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44, Application US/11228659
Publication No. US20060064786A1
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                     Matches
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LOCATION: 2876, 2877, 2878, 2879, 2:
LOCATION: 2886, 2887, 2888, 2889, 2:
LOCATION: 2896, 2897, 2899, 2:
LOCATION: 2996, 2907, 2908, 2909, 2:
OTHER INFORMATION: n = A,T,C or G
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: 2954, 2955, 2956,
LOCATION: 2964, 2965, 2966,
LOCATION: 2974, 2975
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LOCATION: 2915, 2916, 2917, 2918,
LOCATION: 2925, 2926, 2927, 2928,
LOCATION: 2935, 2936, 2937, 2938,
LOCATION: 2935, 2936, 2937, 2938,
LOCATION: 2945, 2946, 2947, 2948,
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LOCATION: (0)...(0)
OTHER INFORMATION: OSI
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ORGANISM: Oryza
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US-11-075-185-36
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CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
DERIOR APPLICATION NUMBER: US 60/568,290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: REEVES, CHRISTOPHER APPLICANT: JULIEN, BRYAN APPLICANT: REID, RALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5679
TYPE: DNA
ORGANISM: Sorangium cellulosum
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Similarity 46.4%;
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

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US-10-819-386A-1
US-10-819-386A-1
US-10-986-2846-30
US-09-861-289-30
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US-10-271-889-48
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	Application US/10611442 No. US20040203015A1 No. US20040203015A1 Hutchinson, C. Richard Katz, Leonard Reid, Ralph Hu, Zhihao Gramajo, Hugo Gramajo, Hugo Gramajo, RECOMBINANT GENES FOR POLYKETIDE VENTION: MODIFYING ENZYMES	RESULT 1  US-10-611-442-2  US-10-611-442-2  Sequence 2, Application US/1061  Publication No. US20040203015A1  GENERAL INFORMATION: APPLICANT: Hutchinson, C. Rich APPLICANT: Ketz, Leonard  APPLICANT: Reid, Ralph APPLICANT: Hu, Zhihao  APPLICANT: Hu, Zhihao  APPLICANT: Gramajo, Hugo  ITITLE OF INVENTION: RECOMBINAN  TITLE OF INVENTION: MODIFYING	~~~~~~~~ G 22
	ALIGNMENTS		
	27541 7 US-10-203-295-2	45 77.6 12.9 27	
411	10056 6 US-10-156-761-411	44 79.2 13.2 10	
	77536 3 US-09-940-316B-1	'n	
28	14055 6 US-10-156-761-2883	4	
3, Appl	9	81 13.5	
15102,	125746 6 US-10-156-761-15102	81.8 13.6	
2885,	ŋ	81.8 13.6	
2882	ŋ	81.8 13.6	
32,	6	84 14.0	
32,	3 US-09-836-821-3	84 14.0	
32,	w	14.0	
32,	w	84 14.0	
32,	220 3 US-09-861-289-	84 14.0	
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34	4689 3 US-09-861-289-34	84.8 14.1	
412	18435 6 US-10-156-761-412	85.2 14.2	
æ	9025608 6 US-10-156-761-1	88.2 14.7	
151	0 6 US-10-156-761-	88.2 14.7	
Sequence 415, App	3238 6 US-10-156-761-415	4 88.2 14.7 2	
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FILE REFERENCE: 300622009100
CURRENT APPLICATION NUMBER: US/10/611,442
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 60/393,016
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 24
SOPTWARR: FRASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 17596
TYPE: DNA
ORGANISM: Micromonospora Megalomicea
PEATURE: ; NAME/KEY: misc\_feature ; LOCATION: (0)...(0) ; OTHER INFORMATION: Genomic DNA US-10-611-442-2 CCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTGGTGATCCGGAGCGGCAG 240 AGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG AGGGACGCCCGGTCGACCTGCCGGTCTACCCCGTTCCAACGACAGAACTTCTGGCTCCCGG TCCCCCTGGGCCGGGTCCCCGACACCGGCGACGAGTGGCGTTACCAGCTCGCCTGGCACC 100.0%; Score 600; DB 8; 1 100.0%; Pred. No. 1.3e-138; vative 0; Mismatches 0; Length 17596; Indels 0 Gaps

Query Match Best Local Similarity

Matches

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Conservative

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GENERAL INFORMATION:
APPLICANT: SANTI, DANIEL V.
APPLICANT: REID, RALPH C.
APPLICANT: KODUMAL, SARAH J.
APPLICANT: KODUMAL, SERASTIAN
TITLE OF INVENTION: SYNTHETIC GENES
FILE REPERENCE: 300622010900
CURRENT APPLICATION NUMBER: US/10/672,396
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US 60/414,085
PRIOR FILING DATE: 2002-09-26
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 9510
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Best Local S
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                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                          Match 31.5%;
Local Similarity 59.5%;
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GTGAAGCGGAATGGGAGTCTGCGTCCCTCGCCGGTCGCGTGCTGCTGGTAACCGGCCCGG
                            ACCCCGTCGACCTCGGGGGGTCCTCCCTGGCCGGACGGGTCCTGGTGACCGGAGCGG
                                                                                       TCC---CCCTGGGCCGGGTCCCCGACACCGGCGACGAGGTGGCGTTACCAGCTCGCCTGGC
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                                                                                                                                                                                                                                                                                                                       Synthetic construct
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                                                                                                                                                                                                                                                          Score 189; DB 7; Length 9510; Pred. No. 1.7e-37;
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APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF
FILE REFERENCE: 3016-202;
CURRENT FILING DATE: 2002-07-26
UNMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 4725
TYPE: DNA
ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-17
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US-10-205-032-17
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Matches 350;
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                                                                                     TGGGTGAGGGACCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGC
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 GCCCGGAGCAGCCGGCGGAGCTGGTCGAGGCGGTGCGCGACGCGCTCACCGCGCGGGGGCG
                            GAGCGGCAGTACCCCCGGCCTGGACGGACGTGGTCCGCGACGGCCTGGAACAGCGCGGGG
                                                            GCTGGCGGCTTCAGCGCACCGGCGCCGCGCCGGCCGACCGGTGGCTGCTGGTGACCG
                                                                                                                        TGGAGCCCGCCGCAGGCGGACTCCGGCCCGGCCGGGACGGCTGGCGCTACCGGGTCG
                                                                                                                                                     rccceerccccreeecceeercccceaca---cceeceaceaereecernaccaecrce
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Pred. No. 1.9e-21;
0; Mismatches 250
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                                                                                                                                                                                                                                                                                                                                       Length 4725;
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; TYPE: DNA
; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-1
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US-10-205-032-1
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CURRENT APPLICATION NUMBER: US/10/205,032
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10205032 Publication No. US20030113874A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAWICIN
                                                                                                                                                                                                                                                                                                                                                                 38933
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                                                                                                                                                                                                                                            TCCCGGTCCCCTGGGCCGGGTCCCCGACA----CCGGCGACGACTGGCGTTACCAGCTCG
CCGAGGTGCGCCTGGTGACCGTCGAGCCGACCAGCACCGGGCCGCGTGCGCGCGT 39292
                                CGACCGTCGTGTTGTGCACCGCGCAGTCG------CGCGCCCCGGATCGGCGCCG 339
                                                                                                    GAGCGGCAGTACCCCCGGCCTGGACGGACGTGGTCCGCGACGGCCTGGAACAGCGCGGGG
                                                                                                                                           GCTGGCGGCGCTTCAGCGCACCGGCGCCGCCGGCCGACCGGTGGCTGCTGGTGACCG
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Pred. No. 1.1e-21;
0; Mismatches 250;
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US-10-203-295-35
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                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Streptomyces noursei ATCC 11455
US-10-203-295-35
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                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their TITLE OF INVENTION: manipulation and utility
FILE REPERENCE: 1181-265
CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: PCT/GB 01/00509
PRIOR PILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0002840.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zotchev, Sergey Borisovich APPLICANT: Sekurova, Olga Nikalayivna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 0009387.2 PRIOR FILING DATE: 2000-04-14
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                                           43960 ACGCCGCACACCGGCGGCGTCCTGGTGCTGGTGCCCGCCGCCGACCACCGACCCCTTGG 44019
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Ellingsen, Tron
Sletta, Havard
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Fjaervik, Epsen
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Strom, Arne Reidar
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US-10-205-032-15
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; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-15
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APPLICANT: Farmet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS FOR
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Best Local Similarity 52.9
Matches 250; Conservative
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CURRENT APPLICATION NUMBER: US/10/205,
CURRENT FILING DATE: 2002-07-26
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APPLICANT: JEONG, Ki Jun
APPLICANT: JEONG, Ki Jun
APPLICANT: ZHOU, XIUPEN
TITLE OF INVENTION: Genes for the Synthesis of FR-008 Polyketides
FILE REFERSUCE: PO03-B015
CURRENT EPLICATION NUMBER: US/10/819,386A
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: KR10-2003-0074035
PRIOR PELING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
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; ORGANISM: Amycolatopsis mediterranei
US-10-042-665A-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/042,665A CURRENT FILING DATE: 2002-01-09 PRIOR APPLICATION NUMBER: 09/242,744 PRIOR FILING DATE: 1999-03-24 PRIOR APPLICATION NUMBER: PCT/EP97/04495 PRIOR APPLICATION NUMBER: PCT/EP97/04495 PRIOR FILING DATE: 1997-08-18 PRIOR FILING DATE: 1997-08-18 PRIOR PILING DATE: 1997-08-18
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APPLICANT: Toupet, Christ
APPLICANT: Engel, Nathal
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ccadeceeccerereedeciceeccedeccercececredaececcrcaacceerees
                               GTGGTGCCTCACTTCCGGCGCGCGGTGAACATCGGCATCCAGGACGCCGTGACCGCACCGG
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                                                                                                                                                                                                            CCTGTCCACTGTGGTCTCTCTGCTGGCGGTGCGGAGGGGGGTGCTGTC---GACGACCC 421
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Engel, Nathalie
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Pred. No. 2.9e-15;
0; Mismatches 220
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APPLICANT: Zhao, L.

TITLE OP INVENTION: DNA encoding methymycin an FILE REFERENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/861,289

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/105,537

PRIOR FILING DATE: 1998-06-26
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; ORGANISM: Streptomyces
US-09-861-289-30
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US-09-861-289-30
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Best Local Similarity
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                                               ceacccaeaccarearceareaccreecceacreareacacareaacreeccecceccec
                                                                                                            CCCTGTGGCTGGTGACCAGGGACGCCGCCGCCGCGGTGACCG----TCGGAGACGACGACGTCGATC
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                                                                                    CCCTGTGGTCCGTCACCCAGGGCGCGGTCTCCGTCGGACGTCTCGACACCCCCGGCCGACC
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ilarity 52.6%;
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Score 89.4; DB 3;
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APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pil
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
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US-09-860-846-30
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; ORGANISM: Streptomyces
US-09-860-846-30
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Xue, Y.
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APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin ar

FILE REFERENCE: 600.536US1

CURRENT PILING DATE: US/09/988,384B

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: PCT/US99/14398

PRIOR FILING DATE: 1999-06-25

PRIOR PILING DATE: 1999-06-25

PRIOR PILING DATE: 1998-06-26

INUMBER OF SEQ ID NOS: 53

SEQ ID NO 30

LENGTH: 13842

TYPE: DNA

ORGANISM: Streptomyces venezuelae
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Best Local
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US-09-836-821-30
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US-09-836-821-30
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CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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Pred. No. 5e-13;
0; Mismatches 271;
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; ORGANISM: Streptomyces venezuelae
US-10-271-889-30
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TITLE OF INVENTION: DA Encoding Methymycin and FILL REFERENCE: 600.582US1
CURRENT APPLICATION NUMBER: US/10/271,889
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/861,289
PRIOR TILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 09/860,846
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-04-17
PRIOR PRIOR APPLICATION NUMBER: US 09/836,821
PRIOR APPLICATION NUMBER: US 09/836,821
PRIOR PILING DATE: 1998-06-26
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US-10-271-889-30
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SOFTWARE: FastSEQ for
SEQ ID NO 30
LENGTH: 13842
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Best Local Similarity
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TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-5
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-09-861-289-5
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CURRENT EPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION UMBER: 09/105,537
PRIOR PILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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; ORGANISM: Streptomyces
US-09-860-846-5
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5
LENGTH: 36778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 317, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA encoding methymycin FILE REFERENCE: 600.438US1 CURRENT APPLICATION NUMBER: US/09/860,846 CURRENT FILING DATE: 2001-05-18 PRIOR APPLICATION NUMBER: 09/105,537 PRIOR FILING DATE: 1998-06-26
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APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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12.0	12.0	12.3	12.3	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.5	12.5	12.9	13.2	13.2	13.3	13.4	13.5	13.7	14.0	14.0	14.1	14.1	14.5	14.9
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ADI23892	ADI23894	ADY72575	ADY72595	AEB86659	AEB86862	ADQ91695	AEB86800	AEB87003	ADQ91711	AAA09469	ADY26824	AAD17184	AAD17185	AAL61224	AAL61172	AAA14651	ADQ74672	ADY80053	AAD54645	ADL91917	AAZ87298	ADL91919	AAZ87299	ADL23088	ABS56090
Adi23892 Streptomy	Adi23894 Streptomy	Ady72575 Polyene p	Ady72595 A. orient	Aeb86659 Streptomy			Aeb86800 Streptomy	Aeb87003 Streptomy	Adq91711 Polyketid	Aaa09469 Streptoco	Ady26824 S. pulver	Aad17184 Streptomy	Aad17185 Streptomy	Aal61224 Actinosyn	Aal61172 Actinosyn	Aaa14651 Nucleotid	Adq74672 Streptomy	Ady80053 Nucleotid	Aad54645 Streptomy	Adl91917 Streptomy	Aaz87298 S. venezu	Adl91919 Streptomy	Aaz87299 S. venezu	Adl23088 Streptomy	Abs56090 S. venezu

### ALIGNMENTS

# RESULT 1 ADI14148 ID ADI1

ADI14148 standard; DNA; 17596 BP.

ADI14148;

15-APR-2004 (first entry)

M. megalomicea cosmid KOS205-57-2.3B SEQ ID NO:2.

ds; polyketide; enzyme; MegR; MegR; MegK; MegCIV; MegBVI; MegBIII; MegL; MegM; megOsamine; megalomicin.

Micromonospora megalomicea.

WO2004003169-A2

08-JAN-2004.

30-JUN-2003; 2003WO-US020681

28-JUN-2002; 2002US-0393016P

(KOSA-) KOSAN BIOSCIENCES INC.

Hutchinson RC, Katz L, Reid R, 품 Ņ Gramajo H;

WPI; 2004-203379/19.

Novel isolated, purified, or recombinant nucleic acid comprising polyketide modifying gene, there gene encodes polyketide modifying enzyme e.g., MegR, MegK, or MegM enzymes useful for producing modified polyketide.

Example 2; SEQ ID NO 2; 51pp; English.

The invention relates to a novel isolated, purified, or recombinant nucleic acid (I) comprising a polyketide modifying gene, where the gene encodes a polyketide modifying enzyme chosen from MegR, MegR, MegK, MegCIV, MegCIV, MegCIV, MegCIV, MegGIV, MegBIII, MegI, and MegM enzymes. A method of the invention is useful for producing a modified polyketide, which involves culturing a recombinant cell comprising the recombinant nucleic acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                Micromonospora megalomicea megalomicin biosynthetic gene cluster
                                                                antiparasitic;
                                                                                                                       21-JUN-2001
                                                                                                                                                                AAF30757
                                                                            Megalomicin;
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 600; DB 12;
Pred. No. 4.3e-85;
; Mismatches 0;
                                                                                                                                                                 ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 6604 G;
                                                                            synthase;
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                                                                            antibiotic;
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            /gene= "megA"
/function= "KS1"
15427. .16476
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/gene= ""megBVI(megT)"T"
deoxyglucose-"
note= "encodes AAB82201"
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/gene= "TDP-megosamine glycosyltransferase"
/product= "TDP-megosamine glycosyltransferase"
/note= "eryCIII homologue; encodes AAB802203"
                                                                  /gene= "meg
/function=
                                                                                                                                                                                                                                                                                                             /gene= "megBII-1(megDVII)"
/product= "TDP-4-keto-6-deoxyhexose
/note= "encodes AAB82299"
complement(9226. .10479)
                                                                                                                                                                                                                                                                                                                                                                  /product= "TDP-4-keto-6-deoxyhexose
/note= "eryVIV, dnmV homolgoue; encc
complement(8228. .9220)
                                                                                                                                                                                                                                                                                                                                                                    complement (8228.
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/genduct= "TDP-4-keto-6-deoxyhexose 3,5-epimerase"
/product= "TDP-4-keto-6-deoxyhexose 3,5-epimerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene= "megDIII"
/product= "daunosaminyl-N,
/note= "eryCVI homologue;
;592. .7197
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/gene= "megDVI"
/product= "TDP-4-keto-6-deoxyhexose
/note= "encodes AAB82202"
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                                                        13849.
                                                                                                    13576.
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'note= "encodes AAB82204"
                                                                                                                                                                 /gene= "megA"
/product= "megalomicin
                                                                                                                                                                                                                                                        'product= "TDP-mycarose glycosyltransferase"
'note= "encodes AAB82210"
complement(10483. .11424)
                                                                                                                                                                                                                                                                                                                                                                                                  gene= "megDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "TDP-3-keto-6-deoxyhexose 3-aminotransaminase"
note= "eryCI, DnrJ homologue, encodes AAB82205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene= "megDII"
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                                                                                                              gene= "megA"
function= "AT-L"
                                                                                                                                                                                                              product= "TDP-4-keto-6-deoxyhexose
note= "encodes AAB82211"
                                                                                                                                                                                                                                   gene= "megBIV"
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                                                                     "megA"
ion= "ACP-L"
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thase; encodes AAB82212"
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encodes AAB82206"
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encodes AAB82208"
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/function= "KR3
26230. .26777
                                                              /gene= "megAIII"
/function= "ACP5"
27393. .28590
/*tag= ab
          /gene= "megAIII"
/function= "KS6"
28897. .29931
                                /gene= "meg/
/function= '
27393. .2859
/*tag= am
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/function= "KS3"
22957. .24237
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/function= "AT1"
17155. .17694
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/function= "KS2"
19876. .20910
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/function= "KR1"
17947. .18207
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/product= "megalomicin 6-deoxyerythronolide B synthase
/note= "polyketide synthase, encodes AAB82213"
22957. .24237
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/function= "ACP3"
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function= "KR5"
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function= "AT5"
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function= "AT3"
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function= "KS5"
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function= "KR2"
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function= "AT2"
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function= "ACP1"
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                                                                                                                                                                                      AGGGACGCCCGGTCGACCTGCCGGTCTACCCGGTTCCAACGACAGAACTTCTGGCTCCCGG
                                                                                                                                                                                                                      CCGCGCTCGCCGAGGCGTACACCCGGGGGGTGGAGGTCGACTGGCGTACCCGCAGTGGGTG
                        CCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTGGTGGTGACCGGAGCGGCAG
                                                                                                                                                        TCCCCCTGGGCCGGGTCCCCGACACCGGCGACACTGGCGTTACCAGCTCGCCTGGCACCC
                                                                                                                                                                                                            CCGCGCTCGCCGAGGCGTACACCCGGGGGGGGGTGGAGGTCGACTGGCGTACCGCAGTGGGTG
                                                                                                                  CCGTCGACCTCGGGCGGTCCTCGCCCGGGCCGGACGGGTCCTGGTGACCGGAGCGGCAG
                                                                                                                                                TCCCCTGGGCCGGGTCCCCGACACCGGCGACGACTGGCGTTACCAGCTCGCCTGGCACC
                                                                                                                                                                              AGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG
                                                                                                                                                                                                                                          100.0%; Score 600; DB 4; llarity 100.0%; Pred. No. 3.6e-85; Conservative 0; Mismatches 0;
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/function= "ACP6"
32257. .32799
/*tag= af
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/function= "TE"
33052. .33312
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/function= "KR4"
32257. .32799
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/function= "KR6"
31396. .32244
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/function= "AT4"
28897. .29931
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/function= "AT6"
29953. .30477
                                                                                                                                                                                                                                                                       /gene= "megAIII"
/product= "megalomicin 6-deoxyerythronolide B synthase
                                                                                                                                                                                                                                                                                                        gene= "megAII"
/function= "ACP4"
                                                                                                                                                                                                                                                                                                                                                                                                                                 gene= "megAII"
/function= "ER4"
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function=
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                   This sequence represents a fragment of the Saccarapolyspora erythraea genome, designated erya. The polypeptides encoded by this region are involved in the biosynthesis of the polyketide segment of erythromycin. eryA is organised in modules and each module takes care of one condensation step. The precise succession of elongation steps is dictated by the genetic order of the modules. This fragment may be specifically altered such that novel polyketide molecules of desired structure are produced. Three types of alteration may be produced; those inactivating a single function in a module which does not arrest acyl chain growth; and those affecting an entire module. The mutations may be introduced by gene replacement. (Updated on 25-MAR-2003 to correct PN introduced by gene replacement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccarapolyspora erythraea; erythromycin; condensation;
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25-MAR-2003
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introduced by gene replacement. (Updated on 2: field.) (Updated on 27-AUG-2003 to correct OS
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(revised)
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elongation; acyl chain growth;
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  25-MAR-2003 to OS field.)
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                                                                                                    ds; gene;
synthetic
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                                  08-APR-2004.
                                                                                                                                     Synthetic polyketide synthase gene method related synthetic
                                                                                                                                                                                    ADM97245;
                                                         WO2004029220-A2
                                                                              Synthetic
                                                                                                                                                             01-JUL-2004
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                                                                                                    polyketide synthase; PCR; medicine;
gene; DEBS3.
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69.7%;
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Pred. No. 2.2e-36;
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26-SEP-2003; 2003WO-US030940

26-SEP-2002;

2002US-0414085P.

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9510 BP; 1587 A; 2635 C; 3236 G; 2052 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New synthetic genes encoding polyketide synthases, useful for facilitating production of therapeutic polyketide compounds, or in and veterinary medicine, pharmacology, agriculture and molecular bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a synthetic gene
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                                                                                                                                                                                                                ATCCGAGTCTCGATGCTCTGGCTTTGGTGCAGGCCCTAGGTGCTGCTGGCGTCGAAGCAC
                                                                                                                                                                                                                                                    ACCCCAGCCTGGACACCCTCGCGTTGGTCCAGGCGCTCGGCGCAGCCGGGATCGACGTCC
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                                                  CGCTGTGGGTCCTGACCCCGTAATGCTGTCCAGGTTGCTGATGGTGAGCTGGTGGATCCTG
                                                                                                                                                          CTGATGCGCTGAGCACCGTAGTATCGCTGTTAAGCCGTG----ATGGCGAGGCTGTCG
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CCCAAGCCATGGTGGGCGGGCTGGGCCGCGTCGTTGGTATCGAACAACCGGGTCGCTGGG
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Pred. No. 4.1e-21;
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                                                                                    Matches 350;
                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                  The invention relates to genes and proteins involved in the biosynthesis of macrolides by microorganisms. In particular it relates to the nucleic acids forming the biosynthetic locus for rosaramicin (a 16-member macrolide antibiotic) from Microomonospora carbonacea. The invention is useful for the biosynthesis of macrolides by microorganisms. It allows direct manipulation of macrolides and related chemical structures by chemical engineering of the proteins involved in the biosynthesis of rosaramicin. It is useful to catalyse certain biochemical reactions, in
                                                                                                                                                                        rosaramicin. It is useful to catalyse certain biochemical reactions, vitro or in vivo, to direct or enhance the synthesis or modification polyketide, polyketide substrate or its precursor. The present sequen is M. carbonacea polyketide synthase (PKS) type I gene. (Updated on 2
                                                                                                                                                                                                                                                                                                                                                                           microorganisms, useful for biosynthesis of preferably for biosynthesis of rosaramicin.
                                                                                                                                       Sequence 4725
                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 164-166; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide involved in biosynthesis of macrolides microorganisms, useful for biosynthesis of macrolides by microorga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cbs
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07-AUG-2003
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                                               CCGCGCTCGCCGAGGCGTACACCCCGGGGGGGTGGAGGTCGACT------GGCGTACCGCAG
  TGGGTGAGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGC 114
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                             CCTCGGCGGCCGAGGCGTTCACCCAGGGGGTGGCCGTGGACTGGTCCCGGGCTCTGGCCG
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                                                                                    Conservative
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(first en
                                                                                                                                       BP; 482 A; 1782 C; 1885 G;
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55.0%;
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.9e-11;
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07-AUG-2003
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(first entry)
                                                                                                                                                                                                                  carbonacea.
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                                    /*tag= d
/product= "Polyketide
5702. .19117
/***
                                                                       4365.
 /product= "Polyketide synthase
19144. .24921
/*tag= f
                                                                                                    complement (2629.
                                                                                                                                 complement (1728. .2522)
                                                                                                                                         partial
                                                                                                                                               /*tag= a
/product= "Polyketide synthase #1"
/note= "CDS does not include start
                                                                                                                                                                                             Location/Qualifiers
                             /*tag=
                                                                                                    /product= "Polyketide synthase
complement(2629. .3861)
                                                                               product= "Polyketide synthase
                                                                                                                                                                                                                                                                                                                                        DNA;
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   CDS
         Novel isolated polypeptide involved in biosynthesis of macrolides by microorganisms, useful for biosynthesis of macrolides by microorganisms, preferably for biosynthesis of rosaramicin.
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P-PSDB; ARE36995, ARE36996, ARE36997, ARE36998, ARE36999, ARE36995, ARE37006, ARE377001, ARE377002, ARE377003, ARE377004, ARE377012, ARE377013.
ARE377008, ARE377009, ARE377010, ARE377011, ARE377012, ARE377013.
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                                                                                                    Yang X,
                                                                                                                                             26-JUL-2001;
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                                                                                                                                                                                                         CA2391131-A1.
                                                                                                                          (ECOP-)
                                                                                                                        ECOPIA BIOSCIENCES INC
                                                                                                    Staffa A,
                                                                                                                                             2001US-0307629P.
                                                                                                                                                                 2002CA-02391131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Polyketide synthase #6" /note= "CDS does not include start /partial 24993. .36230
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/product= "Polyketide
56408. .57634
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49868. .51226
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41049. .46403
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/product= "Polyketide
36292. .41016
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/product= "Polyketide
57657. .59123
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Polyketide synthase #13"
/transl_except= (pos:51221. .51223, aa:Xaa)
note= "Xaa corresponds to amino acids from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19092. .49814
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/product= "Polyketide
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/note= "CDS does not include start
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note= "CDS does not include start codon"
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/product= "Polyketide
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note= "CDS does not include start
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Best Local
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     29-NOV-2001
                             AAD17186;
                                                      AAD17186 standard; DNA; 125401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60196 BP; 6934 A; 20042 C; 23822 G; 9398 T; 0 U; 0 Other;
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     (first entry)
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Pred. No. 3.9e-11;
0; Mismatches 250;
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   The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin.
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Zotchev
Valla S,
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10-APR-2000; 2000GB-00008786
14-APR-2000; 2000GB-00009387
New nystatin polyketide synthase as antibiotics and antifungals.
                                                   WPI; 2001-557614/62.
P-PSDB; AAE10143, AAE10144,
                                                                                                                                (STRO/)
(VALL/)
                                                                                                                                                                      (SEKU/)
(FJAB/)
                                                                                                                                                                                              (UYNO-)
(SNTF)
(ALPH-)
(SINV-)
(DZIE/)
(ZOTC/)
                                                                                                                                                                                                                                                                                                                                           08-FEB-2001;
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                                                                              / SB, Sear.
S. Ellingsen '
                                                                                                                             DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUPOVA O N.
FJAERVIK E.
BRAUTASET T.
STROM A R.
VALLA S.
                                                                                                                                                                                                                       SINTEF STIFTE ALPHARMA AS. SINVENT AS.
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                                         AAE10150.
                                                                                       Sekurova ON
llingsen TE,
                                                                                                                                                                                                                                                              NORGES TEKNISK NATURVITENSKAPELIGE.
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/note= "CDS does not include
complement(60238. .61296)
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34792. .51099
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complement(58786. .58980)
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1155. .57355
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Sletta H,
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             polypeptides, useful
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a Streptor
                                                                                                                                             Micromonospora
                                                                                                                                                                                                   Macrolide;
                                                                                                                                                                                gene;
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                              /product= "Polyketide synthase"
/note= "CDS does not include st
                                                                                                         ocation/Qualifiers
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Pred. No. 5.9e-08;
0; Mismatches 238;
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                                                                                                                                                                                                   polyketide synthase;
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P-PSDB;
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nilarity 52.9%;
Conservative (
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Pred. No. 2.6e
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                                                            /product= "PKS FscB, SEQ ID complement(77983...84132)
/*tag= r
                        /product= "PKS F8cF, SEQ ID 5" complement (84170. .107485)
                                                                                                                                                                                                                                                               /product= "ABC transporter, 27561. .28280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "GDP-ketosugar
18"
                                                                                                                                                                                                                                                                                                                        /product= "PKS FscA,
26333. .27340
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/product= "Glycosyltransferase,
14953. .16011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Regulator protein,
complement(10298. .13315)
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complement(7210. .10320)
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complement(4377..7205)
                                                                                                                                             /product= "PKS FacC, SEQ ID complement(60962. .77587)
                                                                                                                                                                                                       /product= "ABC transporter,
complement(28983. .60860)
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17556. .18413
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complement(3150. .3818)
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18610. .20781
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complement (574. .1950)
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                                                                                                                                                                                                                                     The present invention relates to a gene cluster (ADZ51725) for the CC biosynthesis of FR-008 polyketides derived from Streptomyces sp. FR-008. CC FR-008 polyketide, a hetaene macrolide having aglycone containing 4-CC aminoacetophenone, has antifungal activity and also high toxicity against mosquito larvae, and so is highly useful in agricultural and medical CC fields. The gene cluster comprises the following genes: fscA, fscC, fscB, CC fscF, fscE and fscD, which code for modular polyketide synthase (PKS); CC fscTI and fscTII, which code for ABC transporter proteins; fscRI, fscRII, CC fscRIII and fscRIV genes which code for regulator proteins; fscR which CC codes for cytochrome P450 monoxygenase; fscMI which codes for ferredoxin CC protein; fscTE which codes for thioesterase; fscMI which codes for CDP-ketosugar CC aminotransferase; fscMII which codes for GDP-mannose-4,6-dehydratase; fscC plycosyltransferase; fscMII which codes for GDP-mannose-4,6-dehydratase; fscC which codes for PAD-dependent monoxygenase; pabAB which codes for ADC CC lyase. The genes of the gene cluster of the invention can be used to CC worldy recombinant microorganisms capable of producing PR-008 CC polyketides, also to increase the productivity of the existing FR-008 CC modification.
                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                   Query Match
Best Local (
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P-PSDB; ADZ51726, ADZ51727, ADZ51728, ADZ51729, ADZ51730, ADZ51731, ADZ51733, ADZ51734, ADZ51735, ADZ51736, ADZ51737, ADZ5173 ADZ51739, ADZ51734, ADZ51742, ADZ51743, ADZ51744, ADZ51748, ADZ51746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New gene cluster for the biosynthesis of FR-008 polyketides, useful increasing the productivity of FR-008 polyketides or to produce new 008 polyketide variants.
                                                                                                                                                                                                                                     Sequence 138203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1; 22pp; English.
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(UYSH-)
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UNIV SHANGHAI JIAOTONG.
GGGACGCCCGGTCGACCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGGT
                                                                                                                           CGCGCTCGCCGAGGCGTACACCCCGGGGGGGTGGAGGTCGACTGGCGTACCGCCAGTGGGTGA
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                                  CGACCTGGCCGTGGACACCGAGGCGCTCGGCGCGGTACTCCCGGCCCTCTCCACCTGGCG
                                                                                                                                                                   Conservative
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/*tag= t
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19"
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                                                                                                                                                                                   16.7%;
53.7%;
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                                                                                                                                                                Score 100.2; DB 14; Length 138203;
Pred. No. 1.7e-07;
0; Mismatches 258; Indels 36; G
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ADZ51745,
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                                                /product=
                                                                                                             /product= "|
41373. .516
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
/label= ORF_F
/product= "polyketide synthase"
                                                                                                                                                                                   /label= ORF_C
/product= "po.
                                                                                                                                                                                                                                                                                            product= *polyketide
5550. .30759
                                                                           label=
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                                                                                                                                                                                                                                                                                                                                                                            맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a Amycolatopsis mediterranei rifamycin comprises gene cluster DNA fragment from the present invention. The DNA comprises a DNA region involved directly or indirectly in the custer responsible for rifamycin synthesis, including the adjacent CC DNA regions to the right and left which, by reason of their function in CC connection with rifamycin biosynthesis, qualify as constituents of this crifamycin processes and functional fragments, derivatives or CC constituents of these. The Amycolatopsis mediterranei rifamycin synthesis gene cluster DNA fragment can be used for producing rifamycin, rifamycin cc modifying genes involved in ansamycin or rifamycin rifamycin, rifamycin be used for inactivating or modifying genes involved in ansamycin or rifamycin in activating or can be used for constructing mutant actinomycetes strains from which the can be used for assembling a cc library of polyketide synthases, which can be used for assembling a cc library of polyketides. A hybridisation probe of the invention can be used for identifying DNA fragments involved in the biosynthesis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim Matches 256;
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P-PSDB; AAW52845, AJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amycolatopsis mediterranei rifamycin synthesis produce rifamycin and rifamycin analogues.
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    GTGGTGCCTCACTTCCGGCGCGCGTGAACATCGGCATCCAGGACGCCGTGACCGCACCGGC
                      GTGGCTGGTGACCAGGGACGCCGCCGCCGTGACCGTCGGAGACGACGT---CGATCCGGC 538
                                                                CACCGCGTCGACGCTCGCGCTGGTCCAGGCCCTGGGCGACACCACCACGTCCGCGCCGCCT
                                                                                                                           CCTCACCGGCGTGCTGCTGCTCGCTCTCGACGGCGGCCCGCGGACGCGGAGAT
                                                                                                                                                  CCTGTCCACTGTGGTCTCTGCTCGCGCTCGCCGAGGGCGGTGCTGTC---GACGACCC 421
                                                                                                                                                                                      CGAGGAAGCTTCGCGGGCACAGCTCGCCGAGCAGCTGCGGAACGTCCTGGCGGAGCACGA 13838
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Pred. No. 4.4e-07;
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CC The invention relates to an isolated and purified nucleic acid segment CC comprising a desosamine biosynthetic gene cluster, a fragment or its CC biologically active variant, where the nucleic acid sequence is not CC derived from the eryC gene cluster of Saccharopolyspora erythraea or CC Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, necomethymycin, narbomycin or a combination of these CC compounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins CC are useful for synthesis of methymycin, pikromycin, neomethymycin and CC useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) CC useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) componers. The compounds produced by the recombinant host cells are useful cas biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desosamine and macrolide biosynthetic gene clusters, useful synthesis of methymycin and pikromycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycineomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
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    venezuelae macrolide biosynthetic gene pikAI, SEQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of
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Streptomyces

macrolide biosynthetic protein

(PikR2) coding sequence

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Query Match
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Matches 317
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                                                                                                                                                                                                                                                                                                                                                                          pikromycin,
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CC comprising a desosamine biosynthetic gene cluster, a fragment or its CC biologically active variant, where the nucleic acid sequence is not CC derived from the eryC gene cluster of Saccharopolyspora erythraea or CC Streptomyces antibioticus. The invention also relates to a macrolide CC biosynthetic gene cluster, or fragments thereof. The macrolide CC biosynthetic gene cluster, or fragments thereof. The methymycin, neomethymycin, narbomycin or a combination of these CC compounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins CC are useful for synthesis of methymycin, pikromycin, neomethymycin and CC arbomycin. The alternative termination of polyketide synthesis may be CC useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) CC monomers. The compounds produced by the recombinant host cells are useful as chemically active agents, in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, imminerum-research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36778 BP; 4758 A; 14303 C; 12864 G; 4851 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                      ACGGACTCGTACCGCAGGTCGCCTGGGTCCAGGCGCTCGGCGACGCCGGAATCAAGGCGC
                                                                                                                                                                                                                                                                                                                           ACCCCAGCCTGGACACCCTCGCGTTGGTCCAGGCGCTCGGCGCAGCCGGGATCGACGTCC
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   CCGACCGGGCCATGCTCTGGGGCCTCGGCCGTCGTCGCCCTTGAGCACCCCGAACGCT
                                                                                                                                      CCCTGTGGTCCGTCACCCAGGGCGCGGTCTCCGTCGGACGTCTCGACACCCCCGCCGACC
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Pred. No. 1e-05;
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-GCCCTGGCCACCGGCGACGACTGGCGCTACCGCATCGACTGGA

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                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence encodes a Streptomyces venezuelae pik gene cluster protein which was used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-2001;
18-MAY-2001;
18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.
                                                                                                                                                                                                                                                                                                                          Sequence 36778 BP;
                                                                                                                                                                                                                                                                                                                                                                        exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 48; 362pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman DH, Liu
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(LIUH/)
(XUEY/)
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                                                                                                                                                                CCGCGCTCGCCGAGGCGTACACCCGGGGGGGTGGAGGTCGAGTGC---G
CGGTCCCCCTGGGCCGGGTCCCCGACACCGCGACGACGACGACTGGCGTTACCAGCTCGCCTGGC
                                             CCACGGCCTCCCGGCCCGGTCTGCCCACCTACGCCTTCCAGGCCGAGCGCTACTGGCTCG
                                                                                        GTGAGGGACGCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCC
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52.6%;
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Pred. No. 1e-0
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                                                                                                                                                                                                                                                                                                                                                                                 AAZ87285;
                                                                                                                                                                                                                                                                                                                                                                                                       AAZ87285 standard; DNA; 37948
The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not
                                                                                                                                                                                                                                                Streptomyces venezuelae; ATCC15439
                                                                                                                                                                                                                                                                  hypercholesterolaemia; crop protection
                                                            Desosamine and macrolide biosynthetic gene clusters, useful for, synthesis of methymycin and pikromycin.
                                                                                                                                                                 26-JUN-1998;
                                                                                                                                                                                     25-JUN-1999;
                                                                                                                                                                                                                             WO200000620-A2
                                                                                                                                             (MING)
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DB; AAY77180.
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CC pikromycin, neomethymycin, narbomycin or a combination of these
CC compounds. Recombinant or augmented cells comprising the desosamine
CC and/or macrolide biosynthetic gene clusters are useful for the production
CC of biologically active macrolides. The macrolide biosynthetic proteins
CC are useful for synthesis of methymycin, pikromycin, neomethymycin and
CC useful to prepare novel antibiotics and polyketide synthesis may be
CC useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA)
CC monomers. The compounds produced by the recombinant host cells are useful
CC as biopolymers, e.g., in packaging or biomedical applications, to
CC engineer PHA monomer synthases or to prepare biologically active agents,
CC chronic obstructive pulmonary disease as well as other diseases involving
CC respiratory inflammation, cholesterol-lowering agents to treat asthma,
CC chronic obstructive pulmonary disease as well as other diseases involving
CC respiratory pathogens, as well as variety of organisms, e.g.,
CC respiratory pathogens, as well as variety of organisms, e.g.,
CC respiratory pathogens, as well as viral parastic pathogens, or as crop
CC polyhetides in plants. The present sequence represents the macrolide
CC polyhetides or plants. The present sequence represents the macrolide
CC biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439.
CC (Updated on 15-8EP-2003 to standardise OS field)
                                                                                   Matches
                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, biosynthetic gene cluster encodes proteins which synthesise methymycin,
                                                                                                                                                                                                                                              Sequence 37948 BP; 4901 A; 14718 C; 13311 G; 5018 T; 0 U; 0 Other:
                                                                                   317;
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                                                                                                                           Similarity
CCGCGCTCGCCGAGGCGTACACCCCGGGGGGTGGAGGTCGACTGGCGTACCGCAGTG---
                                                                                   Conservative
                                                                                                                           14.9%;
52.6%;
                                                                                   0;
                                                                                                                           Score 89.4; DB 3;
Pred. No. 1e-05;
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Search completed: April 7, 2006, 03:16:47 Job time: 346.081 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Post-processing: Minimum Match 0%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.4	1.6	2.3	2.8	Query Match Length
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1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.1
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## ALIGNMENTS

	FEATURES BOUICE	AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 CL440273/c LOCUS DEFINITION
/organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /clone="L001 PA_0005_L16" /clone="L001 PA_0005_L16" /clone="bacteria" /clone_lib="pooled genomic library of 12 strains of /clone_noled genomic library of 12 strains of Pseudomonas aeruginosa" /note="Vector: pCR4-TOPO; using TOPO Shotgun method; 12 strains include: 1) 11 isolates from clinical samples of pediatric otitis media with effusion: Pitt 'A', Pitt 'B',	Contact: Shen K Center for Genomic Sciences Allegheny-Singer Research Institute 320 East North Avenue, Pittsburgh, PA 15212, USA Tel: 412 359 5097 Fax: 412 359 5095 Email: kshen@wpahs.org Complete insert sequence Seq primer: M13 Reverse, and T7 Class: shotgun High quality sequence stop: 1521. Location/Qualifiers 11521	Shen, K., Sayeed, S., Hu, F.Z., Antalis, P., Gladitz, J., Ahmed, A., Hayes, J., Johnson, S., Dopico, R., Preston, R.A., Erdos, G., Post, J.C. and Ehrlich, G.D. Sequence from pooled genomic library of 12 isolates of Pseudomonas aeruginosa Unpublished (2004) Other_GSSs: L001_PA_0026_A07	CL440273.1 GI:45577320 CL440273.1 GI:45577320 GSS. Pseudomonas aeruginosa Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas. 1 (bases 1 to 1521)	1521 bp DNA linear GSS 09-APR-2004 L001 PA_0005_L16 pooled genomic library of 12 strains of Pseudomonas aeruginosa Pseudomonas aeruginosa genomic clone L001 PA_0005_L16, genomic survey sequence.

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Burns,J.L., Kaul,R. and Oleen,M.V.
Whole-Genome-Sequence variation among multiple isolates
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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University of Washington
Box 352145, Seattle, WA
Tel: 2062216954
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CG4587.ri Candida glabrata Random
genomic clone CG4587, genomic surv
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Genome Biol. 4 (2), R10 (2003)
                                                                                                                                                                                                Dublin 2, Ireland Tel: 353 1 6082319
                                                                                                                                                                                                                           Department of Genetics,
Trinity College Dublin
                                                                                                                                                                                                                                                      Contact: Wong
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                                                                                                                                                                        Email: swong@tcd.ie
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                                                                                                                                                            plasmid ends.
                                                    /clone=
/clone_
                                                                                                                                            Location/Qualifiers
                                                                                         organism="Candida glabrata"
|mol_type="genomic DNA"
|strain="CBS 138"
                                                                  db_xref="taxon:5478"
clone="CG4587"
                                                                                                                                                                                                                                                                                                                                    1 to 584)
                                                                                                                                                                                                                                                                                                                                                                                                                  GI:24442259
                                                                                                                                   . 584
 1.6%;
                                                   _lib="Candida glabrata
Score 141.6; DB 9; Pred. No. 5.2e-15;
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Genomic Library Candida glabrata
                                                    Random Genomic Library"
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                                                        CGATGCAGTGCCGTACCCCGACCAGGTCGGCGAC 4918
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                                                                                                                                                                                                                                                                                               GCCAGCTCGCCGCGTGCCCGCGCGCGCGAAGGTCATTGACGGCATGATCACTTCACCGG 4830
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Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hasti
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates
Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pacs2-164_3982.x1 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_3982, genomic survey secuence
                                                                                                                                                                                                                                                        Genome Center
University of Washington
Box 352145, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
Bacteria, Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                       Contact: Chris K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
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                                                                                                                                                                                                                  2066857244
                                                                                                                                                                    shotgun.
                                                                                                                                                                                          craymond@u.washington.edu
                                           /organism="Pseudomonas
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164_3982"
/clone_lib="pacs2-164"
                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1628)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
                                                                                                                          Evolutionary Biology
Max-Planck-Institute for Developmental
Spamannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371
Pax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG757066 1628
PD052-2-A02.za Ppa EcoRI BAC I genomic survey sequence.
CG757066 CG757066.1 GI:37985257
                                                                                                                                                                                                                                                                                Mol. Genet. Genomics 269 (5), 12884007
                                                                                                                                                                                                                                                                Contact: Sommer RJ
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
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/db xref="taxon:54126"
/clone\_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

N

1.3%; Score 118.4; DB 10; Length 1628;
t Local Similarity 44.1%; Pred. No. 7.5e-11;
ches 639; Conservative 0; Mismatches 797; Indels 14; Gaps
ches 639; Conservative 0; Mismatches 797; Indels 14; Gaps

7543 CACCGGACCGCCGCCGAGGTGCTCGCCGATCCGGGCTTCACCCACGGCCCGGCCCGACGCT GCCCCCGCCGGGNCGGCGCCGCCGCCGCCGGCCCGGGCCGCGGGGGCGCCGNGGCGCGC TTCTACGCCCGCACCGAGGACGCGGCGTCGGTGAC----AGTGGACGCCGACTGGCTCC ссвесветсвеньсессветветветвенней принцепроводительного станственный принцепроводительного CGCAACAGCTCGCGGTGACCGAACAGGCGCTGACCGCCCTCGACGAGATCGACGCGGTCA CCGACCGTCTCCGGTCCTGGACCTCGGCGACCCCGGGTATGCCTGGACGCCCAGGTCAGCC 7897 TCGCCCGGGAGGTCCCGGTGCTGGGCGCTCGGTACCGCGCCCGCACTCAAGGGCGTGGACC AGCAGCGGTGCGCCAGGCTGGACCGAGCTGGGGTCGCGCTTCGATCTCGTGAACGACT 7957 7777 1433 7717 1493 1553 8017 1193 1313 7837 7662 7602 1253 S

1192 cadella cidad cidad

B GCGAGGTGACAGTCGTCGCCGCGCGGGGGGAACCGCCGAGGTGAACGTCCCGACCGGTG 819

98 GCGAGGTGACAGTGGTCGTCGCCGCGGGGGAACCGTGATCCCGAGGTCTTCACCGATCCCG 8257

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RESULT 6
CC142184
LOCUS
DEFINITION
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AUTHORS
TITLE
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1 (bases 1 to 987)
1 (bases 1 to 987)
1 Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other_GSSs: NDL.80J12.SP6
                                                                                                                                                                                                                                                                                                      CC142184
NDL.80J12.T7 Notre
NDL.80J12, genomic
                                                                        Email: enta@tigr.org
Library was provided
Seg primer: T7
                                                                                                                                                                                                                                                                             GSS
                                                                                                                                                Department of Eukaryotic Genomics
                                                                                                                                                           Contact: Brendan Loftus
                                                                                                                                                                                                                                                     Aedes aegypti
                                                                                                                                                                                                                                                                 Aedes aegypti (yellow fever mosquito)
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CC142184.1 GI:30011239
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                                                                                                                  Medical Center Drive, 301-838-3543
                                                                BAC ends.
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
                                         Location/Qualifiers
j. .987
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AG363333
Mus musculus 1
sequence.
AG363333
AG363333.1 G:
GSS.
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Query Match
Best Local Similarity
GTTCCAGGGCGACGGTGGCGTTGCAGGTGGCGATGCAGTGCCGTACCC
                                                                                   CCGCGAAGGTCATTGACGGCATGATCACCTTCACCGGTGACGTCACCGGCCCGCAGCACCA
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    CACAAATGAATAGGGTGTCGTTATGACTTCACCGGTTATTCTCAATGCTTGAAGTGCGG

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/clone_lib="Notre Dame Liverpool"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
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Pred. No. 2e-10;
0; Mismatches 400;
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molossinus

2332 DNA,

clone:MSMg01-165A22.TJ,

GSS 21-DEC-2004 , genomic survey

Query Match Best Local Similarity 41.4%; Pred. No. 1.1e-09; Matches 898; Conservative 0; Mismatches 1249; Indels 20; Gaps  Qy 2424 CGTCGGCGGACGTCCCGTTCGAGTTGAGCCGGGCGGTCACCGGACTGGTCGAAACCGT	COMPANY  CLORES are defined them the mouse but inlied year of the context to the	AL RS
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concatenation or

jgi.doe

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JG1 CUNH1244.rev NIH XGC tropMet
IMAGE:7762993 3', mRNA sequence.
     DOE Joint Genome Institute Xenopus tropicalis Unpublished (2004) Other_ESTs: JGI_CUNH1244.fwd
                                                                            1 (bases 1 to 847)
Richardson, P., Lucas, S., Rokhsar, D.,
Brokstein, P. and Lindquist, B.A.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos; Silurana.
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DNA Sequencing: DOE Joint Genome Institute: http://www.
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
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Tissue Procurement: Dan
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/lab_host="ElectroMAX DH10B"
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AG381986
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Mus musculu
                                                                                                                                                                                                                                                                                                                     Submitted (17-NOV-2003) Massahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abcertc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 KOyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                      Vector
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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1.2%;
ilarity 42.5%;
Conservative
                                                                                                                /organism="Mus musculus molossinus"
|mol type="genomic DNA"
|sub_species="molossinus"
|db xref="taxon:57486"
|clone="MSMg01-192D21.TJ"
                                                                     /tissue_type="mixture of
/clone_lib="MSMg01 Mouse
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                  sex="male"
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                  TGGCTGTCAACAGCCATCTGTTCGGGCTGGTCCCGCTCGCAAGCGCCTTCCAAGGCGGCCG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
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phone: 81-298-36-9189, fax: 81-298-36-9199
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Shiroishi, T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing : IJ
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                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .2332
                                                                                                                                                             tissue_type="mixture of/clone_lib="MSMg01 Mouse
                                                                                                                                                                                                                                                 /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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Srinivasan, J., Sinz, W., Jesse, T.,
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/strain="California"
/db_xref="taxon:54126"
/db_ref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
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                                                                                                                                                                                                                                                   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Mone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AG441877
AG441877.1
GSS.
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                                                                                                                                                                                                        LIBRARY
                                                                                                                                                                                                                  Sequencing:
                                                                                                                                                                                                                                 PRIMERS
                                                                                                                                                                                                                                          e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Shiroishi, T.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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tori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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(,, Saitou,N., Hattori,M., Sakaki,Y.,
                                                                                                                                                     Location/Qualifiers
                                       tissue_type="mixture of/clone_Tib="MSMg01 Mouse
                                                                                          /sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                              organism="Mus musculus molossinus"
/mol_type="genomic DNA"
                                                                  sex="male"
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Moriwaki, K.
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0; Mismatches 611;
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Best Local Similarity
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Bequence.

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AG430101

AG430101

AG430101.1 GI:48073164

DS GSS.

Mus musculus molossinus (Japanese wild mouse)

Mus musculus molossinus

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;

Mammalla; Eutheria; Murinae; Mus.

"""urina,M., Toyoda,A., Kojima,T.,

Moriwaki,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tenkuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
KOyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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R.Site
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Genome Res. 14 (12), 2439-2447 (2004)
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Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY
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                                                                                                                                                                                                                                                                                            tissue_type="mixture of kidney and spleen"/clone_Tib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                           sex="male"
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Pred. No. 8.5e-08;
0; Mismatches 599;
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Buntjer,J., van der Meulen,M. and Sommer,R.J.

Buntjer,J., van der Meulen,M. and Sommer,R.J.
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/note="The library was generated by a partial digest
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Fujiyama, A., Hattori, M
Totoki, Y., Watanabe, H.
Direct Submission
                                                                                                                                                                        Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                      Unpublished
                                                                                                                                                                    BAC end sequences
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Mammalia; Eutheria;
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                                                                                Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-021B06.R"
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/cell_type="
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Search completed: April Job time : 34756 secs

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1: /SIDSS/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

2: /SIDSS/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

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18 US-11-075-185-2
19 US-10-497-135-17
18 US-11-143-401-127
19 US-11-143-401-127
19 US-11-125-19-1
19 US-11-075-185-2
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13 US-10-858-730-38
14 US-11-075-185-2
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Sequence 1690, Ap
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Sequence 18, Appl
Sequence 18, Appl
Sequence 10202, Ap
Sequence 10202, Ap
Sequence 2, Appli
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Sequence 3, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 35, Appli
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#### ALIGNMENTS

RESULT 1 US-10-506-454-1690/c

Sequence 1690, Application US/10506454
Publication No. US20060068386A1
GENERAL INFORMATION:

APPLICANT: Slesarev, Alexi I
APPLICANT: Slesarev, Katja V
APPLICANT: Polushin, Nikolai N
APPLICANT: Shekhova, Vera V
APPLICANT: Shekhova, Vera V
APPLICANT: Shakhova, Vera V
APPLICANT: Shakhova, Vera V
APPLICANT: Malykh, Andrei G
APPLICANT: Malykh, Andrei G
APPLICANT: Malykh, Andrei G
APPLICANT: Malykh, Andrei G
APPLICANT: Nozyavkin, Sergei A
TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophi.
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogen.
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogen.
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogen.
TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogen.
TURE OF INVENTION NUMBER: US/10/506,454
CURRENT FILING DATE: 2004-08-31
PRIOR APPLICATION NUMBER: 60/361,742
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 1722
SOFTWARE: Patentin version 3.2
SEQ ID NO 1690
LENCTH: 1694969
TYPE: DNA
ORGANISM: Methanopyrus kandleri
US-10-506-454-1690 밁 5 밁 S Query Match 1.4%; Best Local Similarity 50.3%; Matches 155792 4258 4198 TGATCACGTACTGGTAGTTGCTCCTCCTCGTCGGCGGGAGCGAGTGCACGGTGACGCCGC 393; GTACGTCGCGCAGCTCGCTGGTGAGAGCGCGTGGTTGACCCCGGTTGTGCTCCCTGGTCT Conservative 0; Score 128.2; DB 7; Pred. No. 6.7e-17; 0; Mismatches 358; Length 1694969; Indels 30; Gaps 4257 155673 4317 155733

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US-11-143-980-1
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                                               APPLICANT: Wagenaar, Melissa M.
APPLICANT: Graziani, Edmund
APPLICANT: Summers, Mia
APPLICANT: Kulowski, Kerry
APPLICANT: Kulowski, Kerry
APPLICANT: Fong, Kevin
TITLE OF INVENTION: Blosynthetic Gene Cluste
TITLE OF INVENTION: Polyketide
FILE REFERENCE: AM-101426US
CURRENT APPLICATION NUMBER: US/11/143,980
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 60/664,483
PRIOR FILING DATE: 2005-03-23
PRIOR FILING DATE: 2005-03-23
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: He, Min
APPLICANT: Hucul, JG
APPLICANT: Haltli, B
APPLICANT: Hagenaar,
APPLICANT: Graziani,
APPLICANT: Summers,
APPLICANT: Kulowski,
APPLICANT: Pong, Key
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APPLICATION NUMBER: US 60/576,895
FILING DATE: 2004-06-03
R OF SEQ ID NOS: 72
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Haltli, Bradley A.
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; SEQ ID NO 1
; LENGTH: 116856
; TYPE: DNA
; ORGANISM: Streptomyces :
US-11-143-980-1
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                                                         GGGTGGAACTGAAGGTGCTCCTACAGCGGCTGCTCGTCAGGTTC 99484
                                                                                         GCCTGGAGAACCAGGTCGCCCTGGAGGAGATCATCGCCCGGTAC 2130
                                                                                                                                                    GTGCCGCGAGCTCTCCTTCGGGCACGGCGTGCACTTCTGTCTCGGTGCCCCGCTGGCGC 2086
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Pred. No. 1e-15;
0; Mismatches 402;
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; ORGANISM: Sorangium cellulosum
US-11-075-185-53
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CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SOFTWARE: Pater
; SEQ ID NO 53
; LENGTH: 1221
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application US/11075185 Publication No. US20050266434A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: REEVES, CHRISTOPHER APPLICANT: JULIEN, BRYAN APPLICANT: REID, RALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
1845 GGAGGTGTTGCGTTTCCGCCCGGTTCCCCCAGATGCAGCGACCACGACCACGACCACGGCCAC
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Pred. No. 2.4e-15;
0; Mismatches 524;
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APPLICANT: REEVES, CHRISTOPHER D

APPLICANT: REID, RALPH

APPLICANT: REID, RALPH

ITITE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS

FILE REFERENCE: 010099.03

CURRENT APPLICATION NUMBER: US/11/075,185

CURRENT FILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US 60/551,103

PRIOR APPLICATION NUMBER: US 60/551,103

PRIOR APPLICATION NUMBER: US 60/568,290

PRIOR APPLICATION NUMBER: US 60/568,290

PRIOR APPLICATION NUMBER: US 60/568,290

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 61

SOPTWARE: Patentin version 3.3

SEQ ID NO 2

TUDE: DANA

LENGTH: 14172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Sorangium
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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1425 CGCCTTCCCGCTGCCGGTCACGATCGTCGCCGAACGTGCTGCGCCCCGGATGGACCA 1484
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Pred. No. 2e-15;
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RESULT 5
US-10-497-135-17
Sequence 17, Application US/10497135
Publication No. US20050272132A1
GENERAL INFORMATION:
APPLICANT: Biotica Technology Ltd
APPLICANT: Gregory, Matthew A
APPLICANT: Gaisser, Sabine
APPLICANT: Betkovic, Hrvoje
APPLICANT: Moss, Steven
TITLE OF INVENTION: Production of Polyketides and
FILE REFERENCE: 4408-P03444US00
CURRENT APPLICATION NUMBER: US/10/497,135
CURRENT FILING DATE: 2004-05-26
PRIOR APPLICATION NUMBER: GB0216509.0
PRIOR FILING DATE: 2003-07-16
PRIOR FILING DATE: 2003-07-16
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US-11-143-401-74
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PRIOR FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 767
                                                                                           Sequence 74, Application US/11143401 Publication No. US20060002953A1 GENERAL INFORMATION:
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Best Local :
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                         APPLICANT: Behr, Marcel
APPLICANT: Small, Pete
APPLICANT: Schoolnik,
APPLICANT: Wilson, Mic
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       T: Small, Peter
T: Schoolnik, Gary
T: Wilson, Michael A.
INVENTION: Molecular Differences
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; ORGANISM: Mycobacteria tuburculosis
US-11-143-401-74
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CURRENT FILING DATE: 2005-06-01
PRIOR APPLICATION NUMBER: US/10/647,089
PRIOR FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: US/09/894,844
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR APPLICATION NUMBER: 09/318,191
PRIOR APPLICATION NUMBER: 09/97,936
PRIOR APPLICATION NUMBER: 09/97,936
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 137
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Best Local Similarity 49.5%;
Matches 428; Conservative
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  CCCGACCCGGACACGTTCGACCCGTCCCGCAAGATCGGTGGTGCCGCGCAGCTCTCCTTC 2046
                                                                            CCGGCCGACGTCATGGTCAACACCTGGGTGCTCTCGGCCAACCGCGATCCCCTGGCGCAT 1986
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                                      CCGGCCGGTCGCCGGGTGCTGCTGCTGTACGGCTCGGCCAACCGTGA---CGAACGCCAA
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Pred. No. 4e-14;
0; Mismatches 409;
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RESULT 7
US-10-497-135-18
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US-10-497-135-18
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CURRENT APPLICATION NUMBER: US/10/497,135
CURRENT FILING DATE: 2004-05-26
PRIOR APPLICATION NUMBER: PCT/GB03/003230
PRIOR FILING DATE: 2003-07-16
PRIOR APPLICATION NUMBER: GB0216509.0
PRIOR PILING DATE: 2002-07-16
PRIOR PILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: GB0224922.5
PRIOR FILING DATE: 2002-10-25
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Best Local Similarity
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SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 761
TYPE: DNA
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APPLICANT: Gregory, Matthew A
APPLICANT: Gaisser, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moss, Steven
TITLE OF INVENTION: Production of Polyketides
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                                            ACCATCAGCGCCGGCGACAACGTGATCCCGCTCTACTCGACGGCCAACCGCGACCCCGGC
                                                                                           GAGATCCCGGCCGACGTCATGGTCAACACCTGGGTGCTCTCGGCCAACCGCGATCCCCTG
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Gaisser, Sabine
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Pred. No. 2e-13;
0; Mismatches 278;
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RESULT 8
US-11-143-401-127/c
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; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 410;
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Best Local
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APPLICANT: Small, Peter
APPLICANT: Schoolnik, Gary
APPLICANT: Wilson, Michael A.
TITLE OF INVENTION: Molecular Differences Between Species
TITLE OF INVENTION: the M. Tuberculosis Complex
FILE REFERENCE: STAN102CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/318,191
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/097,936
PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/143,401
CURRENT FILLING DATE: 2005-06-01
CURRENT FILLING UNIVERSE: US/10/647,089
PRIOR FILING DATE: 2003-08-21
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 CGAGCTCCTCCCAGACGCTGATCTGGGGGATTGCCGACGCCGAACACATTGGCCAGCAGGA
                             CGATCTTC-GCCAGCGCCTCCACAGGTGCTGGTCGGCCCC-----ACAGGTGTA
                                                             CGTACGTGGAGCCGAAGCCGGCCGACCGAGTCGAGCACAATCGGTAGCTCCCATTCGGCGG
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Pred. No. 1.5e-12;
0; Mismatches 392;
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   AACCGGGCGAGGCCCTCCCGCAACTCGGTCCGTTCGCCCTCGGACAACCTGCCGTCGTCC
                                  TCCAACGCGTAACCCAGGTCGGTCTGCATGCCCGGGGGTCCGCTCGGCGGCGTAGTCGACG
                                                                                              TGGAACAGCGGGACCGCCACGGCCACGGCCAGGTGGTGCCCGGTGCTCCCGGCGGAGGATC
                                                                                                                           CCGGCCGTCTGGAACAGCACGGGCGAGAAGAAGGCGATGACGATGACCCCCGTGAGCTGC
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TEGTIGAGCCAGTTGTTGTTCAGGGCCCACTCCAGGCGGGCCCAGGAACCGCTGCCGGTCGC 5013
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                                                        CGATCGTCGGCCGGCCCACGTGCAGGGGGGGGGCAGGAACGCCTCGGGACC
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CGGGAAAGCTCGGGCGGATGAAGGGGATCTTGGGGATCGTCGAGCCACC
                                                                                                                      AGTTCGTGTACCAGTTAGCCTGGGCGATCTGTACGAAGTCCTCGGCGAGCTCGGCTGGCC
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Sequence 2020, Application US/11096568A
Publication No. US20060048240A1
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandroy, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592FUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20202 Query Match
Best Local Similarity
Matches 447; Conserv LENGTH: 1884
TYPE: DNA
ORGANISM: Zea mays subsp. mays
FEATURE:
FEATURE:
NAME/KEY: misc\_feature
LOCATION: (1)...[1884)
OTHER INFORMATION: Ceres Seq. I 2570 GGGGTGACCCGGCCGACGTAGCGGGGTGGCCCCGGCCAGCCCGGGGAAACCGGCCTCC CGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACCGCCACCTGCGGATGGGCGGTC GAGGCGAGGTTGACGGCGCCGAGGATGACGGCGCCCATGAGCGCGGCGTTGCTGCCGAAC Conservative 1.0%; 0; Mismatches 559; 占 Score 92.6; DB 11; Pred. No. 1.7e-09; no. 12379414 Length 1884; Indels 9; Gaps 1011 2689 1071 2629

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US-11-205-109-1/c
      SEQ ID NO 1
LENGTH: 88421
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/11205109
Publication No. US20050287641A1
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                 FILE REFERENCE: 3002-2US
CURRENT APPLICATION NUMBER: US/11/205,109
CURRENT FILING DATE: 2005-08-17
PRIOR APPLICATION NUMBER: US/09/976,059
PRIOR FILING DATE: 2001-10-15
PRIOR PPLICATION NUMBER: US 60/239,924
PRIOR APPLICATION NUMBER: US 60/239,924
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                  APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos
APPLICANT: Zazopoulos
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
                                                                SOFTWARE: PatentIn
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                                                                  version 3.0
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                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (66546)..(67370)
OTHER INFORMATION: ORF 16;
                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (65826)..(66530)
OTHER INFORMATION: ORF 15;
                                                                             NAME/KEY: misc_feature
LOCATION: (67384)..(700
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (39713)..(65800)
OTHER INFORMATION: ORF 14;
NAME/KEY: misc_feature
LOCATION: (70099)..(706
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (19032)..(39:
OTHER INFORMATION: ORF
FEATURE:
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LOCATION: (15880)..(19035)
OTHER INFORMATION: ORF 12;
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LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10;
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NAME/KEY: misc_feature
LOCATION: (13617)...(12802)
OTHER_INFORMATION: ORF 9;
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LOCATION: (12751)...(10829)
OTHER INFORMATION: ORF 8;
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LOCATION: (9464)..(8130)
OTHER INFORMATION: ORF 6
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                                                                                                                                                                                                                             FEATURE:
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LOCATION: (15591)..(15
OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (4038)..(5048) OTHER INFORMATION: ORF 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMB/KEY: misc_feature
LOCATION: (3118)..(403
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                                                                                                                                                                                                                                                                                                                                                                                                               .(39713)
ORF 13;
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ORF 11;
                                                                                 (70059)
ORF 17;
                       (70662)
  18;
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Query Match  1.0%; Score 92.6; DB 14; Length 88421; Best Local Similarity 42.4%; Pred. No. 1.3e-09; Matches 1317; Conservative 0; Mismatches 1729; Indels 57; Gaps 13;  Qy 2391 CGGCGGGATCAGGCCCGATGCTGATCCCACCGGTCGGCGACGTCCGGTTCGAGGTTGGT 2450	; LOCATION: (87372)(86803); COTHER INFORMATION: ORF 32; negative strandedness; FEATURE; NAME/KEY: misc_feature; NAME/KEY: misc_feature; LOCATION: (87494)(88420); COTHER INFORMATION: ORF 33; positive strandedness; N-terminus only US-11-205-109-1		; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (82587)(84446) ; OTHER INFORMATION: ORF 29; positive strandedness ; FEATURE: ; NAME/KEY: misc_feature	; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (82346)(82062) ; OTHER INFORMATION: ORF 28; negative strandedness	: misc_feature  : (81909)(81682)  FORMATION: ORF 27;	; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (81624)(79861) ; OTHER INFORMATION: ORF 26; negative strandedness	; FEATURE: ; NAME/KEY: misc_feature ; LCCATION: (79864)(78107) ; OTHER INFORMATION: ORF 25; negative strandedness	; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (78110)(76449) ; OTHER INFORMATION: ORF 24; negative strandedness	; FEBTURE: ; NAME/KEY: misc_feature ; LOCATION: (75535)(76464) ; OTHER INFORMATION: ORF 23; positive strandedness	; REATURE: ; NAME/KEY: misc_feature ; LOCATION: (75424)(74213) ; OTHER INFORMATION: ORF 22; negative strandedness	; RAMINE: ; NAME/KEY: misc_feature ; LOCATION: (74216)(73563) ; OTHER INFORMATION: ORF 21; negative strandedness	; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (73439)(71964) ; OTHER INFORMATION: ORF 20; negative strandedness	; FEATURE: ; NAME/KEY: misc feature ; LOCATION: (70659)(71906) ; OTHER INFORMATION: ORF 19; positive strandedness
D	Q B Q B ;	Q B Q B	8 B 8	B &	당 <b>성</b>	B &	D Q	B &	р <b>Q</b>	₽ <b>%</b>	B 8	4g VQ	D Qy
46472 GETGCAGCACCACCACGAGCACGTGCGTCGCCGCGGGGGGGG		46712 CGGGCAGGTCCAGCTCCCGGCACGCCCGTCGAGCCGCCAGTGGGCGATCTGCC 46653  3231 GCCGGGCGGCGTCGACACCAACGCCCCGATACCCGGGTTGGTCAACGGTTCCAGGCCGC 3290	3111 CGTTGTTCAGCCCGTACAGGAGGTACGGACCGCGGCGAGGTCCCACAGGCCGGGCTGGC 3170	3051 GAAGGTTCTTCCTGACCCGTTCGAAGGCGCCACGCTTGCCGGTGGTGGCCTGGTACTCGT 3110	2991 TGTGGTTGAGGCCGAGCCGGACCGGTGCCGCCCGTTCGGCGCGCATCCGGCAGGAAGTCCC 3050	2931 TGAGTTCGGCGATGAAGTCGACCAGGTCGATGAGGCGGTTGGCCCGGCCGG	2871 GACCGCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGCGGCCGGTGGGGCTGGACTCGT 2930	2811 ACCGGGGGAGGCCTCCCGCAACTCGGTCCGTTCGCCCTCGGACAACCTGCCGTCCC 2870	2751 CCAACGCGTAACCCAGGTCGGTCTGCATGCCCGGGGGTCGGCGGGGGGGG	2691 GGCGCATCGTTTCCGGCCGGATCCGCAACAGCTGGGCGTCGACGCCCGACGCGCGCG	2631 GGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACCCCACCTGCGGATGGGCGGTCG 2690	2571 GGGTGACCCGGCCGGCGACGTAGCCGGGTGGCCCCGGCCAGCCCGGGGAAAACCGGCCTCCC 2630	2511 GATCGATGCTGCGGCCCGACGTGACGAAGTCGTGGACGACGACGAGTGCAGGCTCCGGTCCG 2570

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                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/11075185 Publication No. US20050266434A1 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILLING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                      APPLICANT: REEVES, CHRISTOPHER APPLICANT: JULIEN, BRYAN APPLICANT: REID, RALPH
                                                                                                                                                                                    TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FILE REFERENCE: 010099.03
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APPLICANT: O DEALY, GENERAL APPLICANT: Trueheart, Joshua APPLICANT: Trueheart, Joshua APPLICANT: Walbridge, Michael J. APPLICANT: Walbridge, Michael J. APPLICANT: Walbridge, Michael J. APPLICANT: Walbridge, Michael J. APPLICANT: Yorgey, Peter S. TITLE OF INVENTION: METHODS AND COMPOSITION FITTLE RETERENCE: 14184-03001

FILE RETERENCE: 14184-03001

CURRENT APPLICATION NUMBER: US 60/475,000

PRIOR APPLICATION NUMBER: US 60/475,000

PRIOR FILING DATE: 2004-03-00

PRIOR FILING DATE: 2004-03-0

NUMBER OF SEQ ID NOS: 364

SOPTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 2736

TYPE: DNA

ORGANISM: Streptomyces coelicolor
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APPLICANT: Bailey, R:
APPLICANT: Blomquist
APPLICANT: Driggers
APPLICANT: Driggers
APPLICANT: Madden, I
APPLICANT: O'Leary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application US/10858730 Publication No. US20050255568A1
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Madden, Kevin T.
O'Leary, Jessica
O'Toole, George
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Matches 836; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGATCATCTCCAGGGCGTCGTTGATGCCGTGCTCGTGCTGGAGGATGAGGACGTCCCA
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No. US20050287641A1

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SOFTWARE:
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TYPE: DNA
ORGANISM: Actinoplanes sp.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2077)...(3078)
OTHER INFORMATION: ORF 1; P
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NAME/KEY: misc_feature
LOCATION: (9691)..(10761)
OTHER INFORMATION: ORF 7; por FEATURE:
NAME/KEY: misc_feature
LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8; ne
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CURRENT FILING DATE: 2005-08-17
PRIOR APPLICATION NUMBER: US/09/976,059
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/239,924
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 3002-2US
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LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2;
                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
NAME/KEY: misc feature
LOCATION: (9464)...(8130)
OTHER INFORMATION: ORF 6; negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (7703)...(6693)
OTHER INFORMATION: ORF 5; negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4;
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LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3;
                                            NAME/KEY: misc feature
LOCATION: (19032)..(39713)
OTHER INFORMATION: ORF 13;
                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (15591)...(15863)
OTHER INFORMATION: ORF 11;
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LOCATION: (13617)..(12802)
OTHER INFORMATION: ORF 9; negative
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LOCATION: (6665)..(581
                                                                                                                                NAME/KEY: misc_feature
LOCATION: (15880)..(19035)
OTHER INFORMATION: ORF 12;
NAME/KEY: misc_feature
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LOCATION: (39713)...(65800)
OTHER INFORMATION: ORF 14; p
FEATURE:
NAME/KEY: misc_feature
LOCATION: (65826)...(66530)
OTHER INFORMATION: ORF 15; p
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NAME/KEY: misc feature
NAME/KEY: (75535)..(76464)
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LOCATION: (73439)..(71964)
OTHER INFORMATION: ORF 20;
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LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19;
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LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17;
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LOCATION: (66546)..(67370)
OTHER INFORMATION: ORF 16;
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LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25;
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (78110)...(76449)
OTHER INFORMATION: ORF 24;
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LOCATION: (75424)..(74213)
OTHER INFORMATION: ORF 22;
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LOCATION: (74216)..(73563)
OTHER INFORMATION: ORF 21;
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LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18;
                                                    NAME/KEY: misc feature
LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31;
                                                                                                                          NAME/KEY: misc feature
LOCATION: (84481)..(85548)
OTHER INFORMATION: ORF 30;
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LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29;
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LOCATION: (82346)..(82062)
OTHER INFORMATION: ORF 28;
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LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27;
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LOCATION: (81624)..(79861)
OTHER INFORMATION: ORF 26;
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misc_feature (87372)..(86803)
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; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33;
US-11-205-109-1
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Best Local S
Matches 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
GGCCAACCGCGATCCCCTGGCGCATCCCGACCCGGACACGTTCGACCCGTCCCGCAAGAT
                                                                                                                                                    CCAGACGCCCACGGTCGCCGGCCTGGCCGACGCCGCCCCCCACCACGGTCGCCGTTCC
                                                                                                                                                                                                         CATCACCACCACCGTCCTGCTGGGCAACATCGTCCGCACCCTCGACGAGCACCCCGGAGTA 1796
                                                                                                                                                                                                                                                               GCGCACCCTCGACGACGTGGAGGCGGCCAACTTCTCCACAGCGTTGCTGCTCGCGGGGCA 1736
                                                                                                                                                                                                                                                                                                                                               ACGGCGGGCCGACCCCCGGGACGACCTGATCTCCCGGCTGGTGCTGGCCGAGGTCGACGG
                                                                                                                                                                                                                                                                                                                                                                                                    CGAACGCATCATGCAGGTGCTGAACCCCGCTCACCTCCTACCTGCTCGACAGGTGTCGGGA 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCCGGCGTACCTGGTGCCGGCCGGCCGTGGTGGTCCTCGACGAGCTGCCCGTCACGGC 61659
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                                         GCTGGAGCAGGCCGAGATCGACCAGGTCGTGGCCACTGTGGACGGCGGCGCCGCCAACGT
                                                                   GGTCGAGATCCCGGCCGACGTCATGGTCAACACCTGGGTGCTCTC---
                                                                                              GCCCAACCTCATCCCCGAGGACGCGCGCGCACATCACGCCCGGCCTGCTGCCGCTCGTGGA
                                                                                                                        TTTCCGCCCCCTTCCCCCAGATGCAGCGCACCACGACCAGGGCCACCACCGTCGGTGG
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Pred. No. 1.8e-08;
0; Mismatches 625;
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APPLICANT: COLE, STEWART T.
APPLICANT: LEADLAY, PETER F.
APPLICANT: MALL, PAMELA L.C.
APPLICANT: MALL, PAMELA L.C.
APPLICANT: JUNIXIN, GRANT A.
APPLICANT: JUNIXIN, GRANT A.
APPLICANT: JUNIXIN, GRANT A.
APPLICANT: HAYDOCK, STEPHEN F.
TITLE OF INVENTION: THE MYCOLACTONE LOCUS: AN ASSEMBLY LINE FOR PRODUCING TITLE OF INVENTION: NOVEL POLYKETIDES, THERAPBUTIC AND PROPHYLACTIC USES FILE REFERENCE: 03495.0329-01
CURRENT APPLICATION NUMBER: US/11/175,689
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: 10/987,592
PRIOR APPLICATION NUMBER: 60/519,864
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Mycobacterium ulcerans
US-11-175-689-5
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US-11-175-689-5
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Best Local S
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SEQ ID NO 5
LENGTH: 1314
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Local Similarity 46.7%;
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                                              CACAAGCAGTTCGGTGACTGGTCCGGCGCCCTGGTCGACATCCAGATGGACGACCCGACC
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Pred. No. 2.9e-08;
0; Mismatches 469;
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US-11-052-554A-529/c
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; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-529
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Best Local Sim
Matches 629;
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                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn
SEQ ID NO 529
LENGTH: 3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
NUMBER: OF SEQ. ID NOS: 763
                                                                                                                                Local Similarity
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Search completed: April 7, 2006, 03:50:34 Job time: 3417.3 secs This Page Blank (uspto)

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Post-processing: Minimum Match 0%
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2849 TCGGACAACCTGCCGTCGTCCCGACCGCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGC	QY         2789         CGCTCGGCGAGGCGTAGTCGACGAACCGGGCGAGGCCCTCCCGGAACTCGGTTCGCCC         2848	OY 2729 TCGACACCCCGACGCAGGCTCTCCAACGCGTAACCCAGGTCGGTC	Db 9772 GCGACCTGCGGGTGGGCGGGTGGGCCGCATGGTGGCGGGCTTGATCCGCAGCAGTAGCGGCG 9831	9712 AGGTCGGGGAAGCCGGCCTGGGGGTACAGGTACAGGTCGGCGATGGACCTGCACC	OY 2609 AGCCCGGGGAAACCGGCCTCCCGGTACAGGTAGACGTCTCCGAGGAGGTCGATCTGCACC 2668	2549 ACCGAGTGCAGGTCCGGTCCGGGTGACCCGGCGACGTAGCGGGTGGCCCCCGCC	QY 2489 AAGAACTCGTCCCCGGCTGCGGATCGTGCGGCCCGACGTGACGAAGTCGTGGACG 2548	GCGGCGTCGCGCTCCAGCTGGTTCAGGCGGCGGTGACGACCTGATCGAAGCCGTCCATG	Db 9472 GGGGGGATTCGGGGCGGGTGCGGGTCAGCGAGGAAGCCGCGGGCCTCCCAGCCAG	GGGCGGGTCGACGCCGTTCAGACGGCGCGGATCAGGCCCCGATGCTGATCCCACCCGTCG	Query Match 14.6%; Score 1309.4; DB 3; Length 12441; Best Local Similarity 67.7%; Pred. No. 8.4e-284; Matches 1850; Conservative 0; Mismatches 876; Indels 5; Gaps 1;	; LENGTH: 12441 ; TYPE: DNA ; ORQANISM: Streptomyces venezuelae US-09-988-384B-3	PRIOR APPLICATION NUMBER: US 09/105,537 PRIOR FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 53 SEQ ID NO 3	CURRENT APPLICATION NUMBER: US/09/988,384B; CURRENT FILING DATE: 2001-11-19; PRIOR APPLICATION NUMBER: PCT/US99/14398; PRIOR FILING DATE: 1999-06-25	Xue, Zhao, NVENTIO	; GENERAL INFORMATION: ; APPLICANT: Sherman, D.H. ; APPLICANT: Liu, H.	; Sequence 3, Application US/09988384B ; Publication No. US20030073824A1	RESULT 2 US-09-988-384B-3	001 GGAGGTGGAGCACCGGGAGGATCC	9001 GGBGGTCGGGAGGATCC 9024	Qy 8941 GTGGGGTCCGGACGTCGCCACCCGGGCAGAGCTTCCTGCGACTGCTGGCCACCA 9000	Db 8881 GCTGACCTTCGCCGCCCCGATCGCGGCCCGGGTCACCGGAACCCCCGCACGCCCGGATGCT 8940
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APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 13613
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; ORGANISM: Streptomyces
US-09-861-289-3
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US-09-861-289-3
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Best Local Similarity 67.7%;
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                                       GGCCGGTGCGGGCTGGACTCGTTGAGTTCGGCGATGAAGTCGACCAGGTCGATGAGGCGG
                                                                                                                 AGCCCGGGGAAACCGGCCTCCCGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACC
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Pred. No. 8.4e-284;
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RESULT 4	_			QY 4889 GENERIC CURINC CHARCE CHARCE CONTROL C	_		# 709 SIGNIC GARGE GARCANCO CONTROL GARC			Dy 4529 GIANCUGATIC CONCENTRATION CONCENTRAT		12194 GTCGAAGCTGGAAGTTGTGGAGGGCGGGGAGCGGGGGGGG	12134 GGCGGCGGCCTCGCTCATCGTCGGGATCCCGCCGGCGGGGCTGCCCGTCGTCGTCACCAGCAGCGGGCTGCCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT		4229 GEGGGAGGGAGGGAGGTCACGCCGCGGAGGAGGTCCACGCGAGGTGAGGCGAGGTGAGCCCCAT	11954 GATGCCGGTGGCCTCGTCGACGATCACGTACTGGTCGTTGTTGAGGCCGTG	, 11	Db 11834 GTGCGGCAGGGCGTGCGGGCGCGCGCGGGAGGATCGCCTGCAGGGTCACGGTC 4168

	QY 2969 TTGGCCCCCCGGCAGGATGATGTGGTTGAGGCCGAGCCGGACCGGTGCCGCTTCG 3028	QY 2909 GGCCGGTGCGGCGACCTCGTTGAGTTCGGCGATGAAGTCGACCAGGTCGATGAAGGCGG 2968	Qy 2849 TCGGACAACCTGCCGTCGTCGCGACCGCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGC 2908	QY 2789 CGCTCGGCGGCGTAGTCGAACGGAACCGGGCGAAGGCCCTCCCGCAACTCGGTCCGCC 2848	OY 2729 TCGACACCCCGACGCACGCCTCCAACGCGTAACCCCAGGTCTGCATGCCCGGGGTC 2788	QY 2669 GCCACCTGCGGATGGGCGGTCGGGCGGATCGGTTTCCGGCCGG	QY 2609 AGCCCGGGGAAACCGGCCTCCCGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACC 2668     -	Qy 2549 ACCGAGTGCAGGCTCCGGGTCACGGGTGACCGGCCGGCTAGCGGGTGGCCCCGCC 2608	QY 2489 AAGAACTCGTCCCCGGCTGCGGATGGATGCTGCGGCCCGACGTGACGAAGTCGTGGACG 2548	Qy 2429 GCGACGTCCCGTTCGAGTTGGTTGAGCCGGGCGGTCACCGACTGGTCGAAACCGTCGAGG 2488	QY 2369 GGGCGGGTCGACGCCGTTCAGACGGCGGGATCAGGCCCCGATGCTGATCCCACCCGTCG 2428	Query Match 14.6%; Score 1309.4; DB 3; Length 13613; Best Local Similarity 67.7%; Pred. No. 8.4e-284; Matches 1850; Conservative 0; Mismatches 876; Indels 5; Gaps 1;	(X)	PRIOR FILING DATE: 1998-06-26  ; NUMBER OF SEQ ID NOS: 43  ; SOFTWARE: FastSEQ for Windows Version 3.0  ; SEO ID NO 3	FILE REFERENCE: 600.438US1 ; CURRENT APPLICATION NUMBER: US/09/860,846 ; CURRENT FILING DATE: 2001-05-18 ; PRIOR APPLICATION NUMBER: 09/105.537	APPLICANT: Liu, H.; APPLICANT: Xue, Y. APPLICANT: Xue, Y. APPLICANT: Xue, L. TITLE OF INVENTION: DNA encoding methymycin and pikromycin	US-09-860-846-3 ; Sequence 3, Application US/09860846 ; Patent No. US20020164742A1 ; GENERAL INFORMATION:
Qy 4109 GAAGTAGGCCTTGCGACGACCACGCGCAGGATCGCCGTCACGGTC 4168	Qy 4049 CTGTGTCAGCCGCAGCGGTGGCCCGTGCCGTAGGGCGTCATCTGGTGGCAGCGGGCGA 4108	p.	. 11 3	3869 CTTCTGGCGTGTGGTGCGAGGATCACGAACCGTTGCGTTTCCGCTTGTCCCACTCCGC	Qy 3809 TCCGCGATCTCCGTCGGTACGGCGGTACGCCGTAGGAGTCTTCATCGACGTACCGAACC 3868	QY 3749 GTGACCTCGGCGCTGAGCGCCCGCACCACGACCGCCGGCCG	Oy 3689 AGTTCGGCGAGCCGGACCGCCTGTCGGTCGGTGTCGGATGCGGCACCGGTGAGGCGG 3748	629 419	3569 CCAGCTGCGGGATGCAACCAGGTCGAGCAGCTCGCCGAACCCGGCCCGGTCCAGG	OY 3509 TTCAGCGGCCTGATCGTGTTGCTCCAGTACTTGCCCGGGGGCCCTGCTCCACCGCCGTG 3568		3389 11179	Qy 3329 TCGTCGATGACCGAGGTGAGGATCTCGTTGCCGGGGCACCCACC	OY 3269 TIGGTCAACGGTTCCAGGCCGCCGGAGAGGTACATCGCCGTCGGGTTCTCCGACGGCACC 3328	Qy 3209 TAGACGGTCAGGGCGAAGCCCCGCCGGGGGGGGGGGGGG	Oy 3149 AGGTCCCACAGGCCGGGCTGGCGCACGCTTGTTCGGTGAGGGCGAAGGCCTTGGTG 3208	QY 3089 CCGGTGGTGGCCTGGTACTCGTCGTTCAGCCCGTACAGGGAGGTACGGACCGCGCCG 3148

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                                                                                                                   RESULT 5
US-09-836-821-3
Sequence 3, Application U
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Publication No. USZ003008
FARRAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
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TITLE OF INTENTION: DNA encoding methymycin an
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: U8/09/836,821
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR PILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
SEQ ID NO 3
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                                                                  GTCGCCGATCGTCGGCCGGCCCACGTGCAGGGGGTGCAGGAACGCCTCGGGACCGCCGAA
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RESULT 6
US-10-271-889-46
; Sequence 46, Application US/10271889
; Publication No. US20030194784A1
; GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
; APPLICANT: Zhao, L.
; TITLE OP INVENTION: DNA Encoding Methymycin an; FILE REFERENCE: 600.582US1
; CURRENT APPLICATION NUMBER: US/10/271,889
; PRIOR APPLICATION NUMBER: US 09/861,289
; PRIOR FILING DATE: 2001-05-18 and Pikromycin

GAATGCGAGGTCGGATAAGGCGCTTTTCACG

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; PRIOR APPLICATION NUMBER: US 09/860,846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/836,821
; PRIOR APPLICATION NUMBER: US 09/105,537
; PRIOR APPLICATION NUMBER: US 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 55
; SOPTWARE: FRAELSEQ for Windows Version 4.0
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Pred. No. 8.4e-284;
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Sequence 3, Application US/10398605
Publication No. US20040161839A1
GENERAL INFORMATION:
APPLICANT: Liu, H.
APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: Chao, L.
APPLICANT: Regents of the University of Minnesota
APPLICANT: Regents of the University of Minnesota
TITLE OF INVENTION: Method to alter sugar moieties
FILE REFERENCE: 600.475US1
CURRENT APPLICATION NUMBER: US/10/398,605
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: PCT/US01/31255
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/238,185
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US-10-398-605-3
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US-10-398-605-3
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows
SEQ ID NO 3
LENGTH: 13613
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Best Local Similarity
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Sequence 1, Application US/10205032

Publication No. US20030113874A1

GENERAL INFORMATION:

APPLICANT: Farnet, Chris

APPLICANT: Yang, Xianshu

APPLICANT: Yang, Xianshu

APPLICANT: Staffa, Alfredo

TITLE OF INVENTION: GENES AND PROTEINS FOR THE

FILE REFERENCE: 3016-2US

CURRENT APPLICATION NUMBER: US/10/205,032

CURRENT FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 60196

TYPE: DNA

ORGANISM: micromonospora carbonacea subspecie

US-10-205-032-1
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                                                                                            GTCCCGGATGAC 55989
                                                                                                                             GACCAGGAGGGC 5511
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GENERAL INFORMATION:
APPLICANT: Meiji Seika Kaisha, Ltd.
TITLE OF INVENTION: Midecamycin biosynthetic ge:
FILE REFERENCE: 138451 US
CURRENT APPLICATION NUMBER: US/10/229,148B
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 210516/2002
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US20040091975A1
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TYPE: DNA
ORGANISM: Streptomyces mycarofaciens
FEATURE:
NAME/KEY: CDS
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LOCATION: Complement((1168)..(2202))
OTHER INFORMATION: ORF41
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                                                                                                                   NAME/KEY:
LOCATION:
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LOCATION: Complement((6048)..(6629))
OTHER INFORMATION: ORF37
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LOCATION: Complement((2220)..(3215))
OTHER INFORMATION: ORF40
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LOCATION: Complement((6653)..(7945))
OTHER INFORMATION: ORF36
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OTHER INFORMATION: ORF39
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NAME/KEY: CDS
PEATURE:
                                                                                                       NAME/KEY: CDS
LOCATION: Complement((13016)..(14044))
OTHER INFORMATION: ORF30
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LOCATION: (9328)..(10458)
OTHER INFORMATION: ORF33
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LOCATION: (9012)..(9335)
OTHER INFORMATION: ORF34
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OTHER INFORMATION:
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                                 LOCATION: Complement OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: CDS
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                                                     Complement ((14074) . . (15096))
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ORF35
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PEATURE:
NAME/KEY: CDS
LOCATION: (48712)..(
OTHER INFORMATION: O
FEATURE:
NAME/KEY: CDS
LOCATION: (59850)..(
OTHER INFORMATION: O
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NAME/KEY: CDS
LOCATION: (19063)..()
OTHER INFORMATION: O
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LOCATION: (64687)...
OTHER INFORMATION:
              FEATURE:
                                          NAME/KEY: CDS
LOCATION: (71113)..(72360)
OTHER INFORMATION: ORF7
                                                                                                       NAME/KBY: CDS
LOCATION: (70365)..
OTHER INFORMATION:
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LOCATION: (42823)..(48657)
OTHER INFORMATION: ORF2
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LOCATION: (29244)...
OTHER INFORMATION:
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NAME/KEY: CDS
LOCATION: (27937)...(28983)
OTHER INFORMATION: ORF18
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NAME/KEY: CDS
LOCATION: Complement((26180)..(27391))
OTHER INFORMATION: ORF19
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LOCATION: Complement((25647)..
OTHER INFORMATION: ORF20
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LOCATION: Complement((24460)..
OTHER INFORMATION: ORF21
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LOCATION: Complement((23555)..
OTHER INFORMATION: ORF22
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NAME/KEY: CDS
LOCATION: Complement((22534)...
OTHER INFORMATION: ORF23
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NAME/KEY: CDS
LOCATION: Complement((20307)..(21743))
OTHER INFORMATION: ORF25
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LOCATION: Complement((17522)..(18895))
OTHER INFORMATION: ORF27
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OTHER INFORMATION: ORF28
 OCATION:
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(72400) . . (73665)
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ORF5
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ORF6
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ORF4
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ORF3
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; OTHER INFORMATION: US-10-229-148B-1
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Best Local 9
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LOCATION:
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LOCATION: Complement((75899)..(76570))
OTHER INFORMATION: ORF10
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NAME/KEY: CDS
LOCATION: Complement((83495)..(84142))
OTHER INFORMATION: ORF16
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LOCATION: (82760)...(
OTHER INFORMATION: C
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LOCATION: Complement((79391)..(81052))
OTHER INFORMATION: ORF13
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LOCATION: (78039)...(
OTHER INFORMATION: C
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LOCATION: Complement((76602)..(77765))
OTHER INFORMATION: ORF11
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OTHER INFORMATION:
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ACGAACCGGGCGAGGCCCTCCCGCAACTCGGTCCGTTCGGCCCTCGGACAACCTGCCGTCG
                                                                                                                                CTCTCCAACGCGTAACCCAGGTCGGTCTGCATGCCCGGGGGTCCGCTCGGCGGAGTCG
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ilarity 65.5%;
Conservative
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ORF12
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ORF17 (
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ORF15
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ORF9
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Pred. No. 5e-260;
D; Mismatches 93
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Publication No. US20030148469A1
GENERAL INFORMATION:
APPLICANT: ASHLEY, GATY
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
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APPLICANT: TANG, Li
APPLICANT: TANG, Li
TITLE OF INVENTION: COMBINATORIAL POLYKETIDE LIBRARIES PRODUCED USING A MODULAR
TITLE OF INVENTION: PKS GENE CLUSTER AS SCAPFOLD
FILE REFERENCE: 300622002103
CURRENT EPLLICATION NUMBER: US/10/201,365
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/141,908
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
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SEQ
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Best Local Similarity 68.1%;
Matches 1015; Conservative
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RESULT 12
US-10-160-539-24/c
; Sequence 24, Application US/10160539
; Publication No. US20030162262A1
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: HETLACH, Mary C.
; APPLICANT: MCDANIEL, ROBERT
; APPLICANT: MCDANIEL, ROBERT
; APPLICANT: TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE
; FILE REFERENCE: 300622002120

SYNTHASE

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PRIOR APPLICATION NUMBER: US/09/657,440
PRIOR FILING DATE: 2000-09-07
PRIOR PPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: CIP OF 09/141,90
PRIOR FILING DATE: 1998-08-28
PRIOR PRIOR FILING DATE: 1998-08-28
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; ORGANISM: Streptomyces
US-10-160-539-24
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Best Local Similarity
Matches 1015; Conserv
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/09/657,440
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                                                         CCGGTGGTCTGCTCGTACTCCTCGTCGTTGAGGCCGTAGAGCGAGGTGCGGATGGCGTGC
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                                                            gcdaggercregccdacgdcgregacccccadarcddcreccddgcreccdd
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US-10-468-828-24/c

| Sequence 24, Application US/10468828 |
| Sequence 24, Application US/10468828 |
| Publication No. US20050026244A1 |
| GENERAL INFORMATION: APPLICANT: BETLACH, Melanie C. |
| APPLICANT: BETLACH, Melanie C. |
| APPLICANT: MCDANIEL, ROBERT |
| CURRENT PELLOATION NUMBER: US/10/468,828 |
| CURRENT PELLOATION NUMBER: US/10/468,828 |
| CURRENT PILING DATE: 2003-08-22 |
| PRIOR APPLICATION NUMBER: US/10/468,828 |
| PRIOR PILING DATE: 2001-02-22 |
| PRIOR APPLICATION NUMBER: US/10/557,440 |
| PRIOR APPLICATION NUMBER: US/10/577,440 |
| PRIOR APPLICATION NUMBER: US/10/577

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; PRIOR FILING DATE: 1998-05-28; NUMBER OF SEQ ID NOS: 39; SOFTWARE: PATENTIN Ver. 2.0; SEQ ID NO 24; LENGTH: 1565; TYPE: DNA ; ORGANISM: Streptomyces venezue US-10-468-828-24
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US-10-846-335-24/c

US-10-846-335-24/c

\$ Sequence 24, Application US/10846335

Publication No. US20050233431A1

\$ GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: HEDANIEL, Robert
APPLICANT: TANG, Li

TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE
FILE REFERENCE: 30062200212

CURRENT FILING DATE: 2004-05-14

PRIOR APPLICATION NUMBER: US/10/846,335

CURRENT FILING DATE: 2001-02-22

PRIOR FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: US/99/793,708

PRIOR APPLICATION NUMBER: US/99/57,440

PRIOR FILING DATE: 1990-05-07

PRIOR APPLICATION NUMBER: US 09/657,440

PRIOR APPLICATION NUMBER: US 09/320,878

PRIOR APPLICATION NUMBER: US 09/073,538

PRIOR APPLICATION NUMBER: US 09/073,538

PRIOR APPLICATION NUMBER: US 09/073,538

PRIOR APPLICATION NUMBER: US 60/134,990

PRIOR SEQ ID NOS: 38

SOFTWARE: PAtentin Ver. 2.0

SEQ ID NO 24

LENGTH: 1565

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Sequence 9, Application US/09861289; Patent No. US20020110897A1; GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Chao, Y.
APPLICANT: Chao, Y.
APPLICANT: Chao, Y.
ITILE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600,438US1; CURRENT APPLICATION NUMBER: US/09/861,289; CURRENT FILING DATE: 2001-05-18; CURRENT FILING DATE: 1998-06-26; NUMBER OF SEQ ID NOS: 43
PRIOR APPLICATION NUMBER: 09/105,537; PRIOR FILING DATE: 1998-06-26; NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 9; LENGTH: 1458; TYPE: DNA CRANISM: Streptomyces venezuelae
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Best Local Similarity 69.5%;
Matches 980; Conservative
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                                                                        GCGGGCGGTGACGACCTGATCGAAGCCGTCCATGAAGTACTCGTCGCCGTCGACGGCCGC
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FTGCTCCA 3534	3475 CCGCCGTACCGCAGCCTCCAACGCGCCGCGGCGGCGTTCAGCGGCCTGATCGTGTTGCTCCA
RECEGECTC 3474        RACEGECTT 376	3415 ACAGCGGAACATGCACGTCGGGCCGGGGTAGAGCCCGACGCTGTACGGGAAGGCGGGCTC
CAGAAGTG 3414          CAGAAGTG 436	3355 GTTGCCGGGCACCACCGACTCCGCGTCGTACTTGGCACCCTGTCACCCGTACGCAGAAGTG
AGGATCTC 3354         AACATGGC 496	3295 GAGGTACATCGCCGTCGGGTTCTCCGACGCACCTCGTCGATGACCGAGGTGAGGATCTC
CCGCCGGA 3294          CCGCCGGA 556	3235 GGCGGCGTGCGACACCAACGCCCCGATACCCGGGTTGGTCAACGGTTCCAGGCCGC
CCCCGCCG 3234	3175 CAGCGTCTGTTCGGTGAGGGCGAAGGCGTTGGTGTAGACGGTCAGGGCGAAGCCCCGCCG
TGGCGGCG 3174       TGGCGCTC 676	3115 GTTCAGCCCGTACAGGGAGGTACCGGACCGCCGAGGTCCCACAGGCCGGGCTGGCGGCG 
TCGTCGTT 3114          TCCTCGTC 736	3055 GITCITCCTGACCCGITCGAAGGCGCCACGCTTGCCGGTGGTGGCCTGGTACTCGTCGTT 
TCCCGGAG 3054       CGGCGCAG 796	2995 GTTGAGGCCGAGCCGGACCCGGTGCCGCCCGTTCGGCGCGCATCCGCAGGAAGTCCCCGGAG
ATGATGTG 2994         ACGATGTA 856	2935 TTCGGCGATGAAGTCGACCAGGTCGATGAGGCGGTTGGCCCCCCCGCCAGGATGATGTG
TCGTTGAG 2934        TCGTTGAG 916	2875 GCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGCGGCCGGTGCGGGCTGGACTCGTTGAG 
TCCCGACC 2874            TCACGGCC 976	2815 GGCGAGGCCCTCCCGCAACTCGGTCCGTTCGCCCTCGGACAACCTGCCGTCGTCCCGACC
ACGAACCG 2814      TCGAAGGC 1036	2755 CGCGTAACCCAGGTCGGTCTGCATGCCCGGGGGTCCGCTCGGCGGCGTAGTCGACGAACCG
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GTCGGGCG 2694            GTGGGCCG 1156	2635 CAGGTAGACGTCTCCGAGCAGGTCGATCTGCACCGCCACCTGCGGATGGGCGGTCGGGCG
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Search completed: April 7, 2006, 04:36:08 Job time: 6273.93 secs

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Post-processing: Minimum Match 0%
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(c) 1993 - 2006 Biocceleration Ltd.
                                            US-08-576-626A-1
US-09-105-537-7
US-09-120-878-21
US-09-141-908-11
US-09-657-440-21
US-09-758-759-3
US-09-758-759-3
US-09-758-759-1
US-09-758-759-1
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
PILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                         NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8051 base pair
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Summers, R.G. APPLICANT: Katz, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2, Application US/08576626A
                                   nucleic acid
DEDNESS: single
                                                                              8051 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                  linear
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3288 CGCCGGAGAGGTACATCGCCGTCGGGTTCTCCGACGGCACCTCGTCGATGACCGAGGTGA 3347	Qy         3228         CCCGCCGGGGGGGGGGGACACCAACGCCCGATACCCGGGTTGGTCAACGGTTCCAGGC         3287         CCCGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5 5 i	4 55 1	Oy       3048       CCCGGAGGTTCTTCCTGACCCGTTCGAAGGCGCCACGCTTGCCGGTGGTGGTGCTGGTACT 3107       107       107       108       107       108	4 5 40 41 57	57	<b>.</b>	ω tπ t	וט ע	QY         2688 TCGGGGCGTCGTTTCCGGCCGGATCCGCAACAGCTGGGCGTCGACGACGCCGGACGAGGC 2747         Y	376	Oy         2568         COGGGGTGACCOGGCGGCGACCTAGCCCCGCCAGCCCGGGGAAACCCGGCCT 2627         4	618	6244	6304		7445 Db	Query Match 33.9%; Score 3032.6; DB 2; Length 8051;  Best Local Similarity 80.2%; Pred. No. 0;  Matches 3529; Conservative 0; Mismatches 866; Indels 6; Gaps 2;  Qy 3348
43	4308 TCCCTGGTCTCGGCGAACGCGTCGAGGGAAGGCCCATCGCCGCGCGCACTCGCTC	5524 GATATGCCGCGCACGTCGCGGAGCTCGTCGGAGTAGAGCGCGTTGAGGGCGGTTGTTGAGGCGGTTGTTGAGGCGGTTGTTGAGGCGGTTGTTGAGGGCGGTTGTTGAGGGCGGTTGTTGAGGCGGTTGTTGAGGGCGGTTGGTT		1111	4068 5704 4128	TOTAL CONTROL CONTRO		3048 GETGETGAGAACGGTTGAGATGACGACGACGAGGGGTGATGAGCACGAGGGGGGGG	3888 GAGGATCACGACTTGCGACTTGCCACTCCGCGTTGATCAACGCACCGCTG	1828 CGGCGCTGCGGTGGGGTCGTCTTCATCGACGTGCGAACCCTTCTGGGGGTGGGT			1618 GOTTO ANGEST GANGE					6484 3348

Db Qy	gb Qy	g Qy	B 8	g <i>Q</i> y	р Q	Db Qy	g Q	D Q	D Q	₽ &	p Q	р <b>Q</b>	B &	D Q	р Q	B 8	d Q
5448 CCGCCTCGGTGCGCAGGTGCACGAGC 	5388 CGGTGTAGTTGTCCGGCTGACAGTGC	5328 GGGTACGCGGGACGTCCAGCACGTAG	5268 GGTTCTCGTTGCGGTAGAACCGCCCA 	5208 ACCGGTGGTCGGGGGGCACCGCCGTCGGGGGGGACTGGCGGACTGGCGGACGGCACTGGCGGA	5148 GCTGGATGTTGACGTAGTGGCTGTGC	5088 ACGCGCTTCACGCCGCCGCCGGTTG	5028 CCCACGTGCAGGGGGTGCAGGAACGC	4968 TIGITCAGGGCCCACTCCAGGCGGGC	4908 AGGTCGGCGACCCGGGCCTCGAACTC	4848 AGCACCAGTTCCAGGGCGACGGTGGC	4788 GCGGTGGCCGCGAAGGTCATTGACGG	4728 CCGGTCGCCGGGTCGACGAA	4668 CCGACGATCGCGCCGGTCTGCGGGGTT	4608 TGGTCGGCGGCGATCTTCGCCAGCGC	4548 GGACGTCCACCCGTCGTGCAGCCCAG	448B GCGGTGACCGCCTTGGTGGCGTGGAA	4428 ATGGCCCGGATCCGTTCGGCCAGCAG
CCGCCTCGGTGCGCAGGTGCACGAGGGCGTGGAGGGTGCCGTCGATCTCCTTGACCAGGA	CGGTGTAGTTGTCCGGCTGACAGTGCACCGTCGCCCGCCAACTCGGCGACGTCGTGGCCAC	GGGTACGCGGGACGTCCAGCACGTAGTCGAGGTAGTCGGGCGGTGTTCCTCGGGCACGT	GGTTCTCGTTGCGGTAGAACCGCCCCACCTCCTCGGAGTGCCAGGCGTCGTAGCGGATCT	ACCGGTGGTCGGGGGCACCGCCGTCGTCGAAGTCCGCGGGCACCTCGACCATGTACC	GCTGGATGTTGACGTAGTGGCTGTGCGCGAGCAGTTCGGTGATCTGGCCGAAGGTCATCC	ACGCGCTTCACGCCGTCGCCGGTTGTAGACGGCCGAGGCGAGGCGAGGCGAGGCTGCGCA	CACGTGCAGGGGGTGCAGGAACGCCTCGGGACCGCCGAAGATCGCCAGATCGGTCGG	CCCACTCCAGGCGGGCCAGGAACCGCTGCCGGTCGCCGATCGTCGGCCGG	AGGTCGGCGACCCGGGCCTCGAACTCCCGGACCAGGGGCCCGCCGTTGGTGAGCCAGTTG	AGCACCAGTTCCAGGGCGACGGTGGGGTTGCAGGTGGCGATGCAGTGCCGTACCCCGACC	.cgcgaaggtcattgacggcatgatcacttcaccggtgacgtcaccggcccgc 	CGCCGGGTCGACGTCGCAGAACACCGGTGTGAGTCCGAGCCAGCTCGCCGCGTGC	CGCCGGTCTGCGGGGTGACGAGCGCGACGTGGTCCGGGTCGACCAGA	ICGATETTCGCCAGCGCCTCCACAGGTGCTGGTCGGCCCCACAGGTGTACG 	CAGGGCGTGGGCGCGTCGAAGAAGACTTGACCTGG	CCGCCTTGGTGGCGTGGAAGCTGAACACCTCGGCGTCACCGGATCCGCCCACC	ATGGCCCGGATCCGTTCGGCCAGCAGCAGCCGTCGTCGTGACCACCGCCCCCCCC
5507 Db	5447 Db	5387 Db	5327 Db	5267 Oy 4505 Ob	5207 4565	5147 4625	5087 4685	5027 4745	4967	4907 Db	4847	4787	4727 5045	4667 5105	4607 5165	4547 5225	. 4487 5285
3244 GAATCGTCCGGTCGGCCGATCACCCATCGCCTCCCTGCGGTCGTCGACGGCT 3185	TOSCOSTI CASTANTA CONTROLO CON	3364 GCGCCCACCTCGAGCCCTGGCGCCCTTGCGGGTCAGCCAGTCGTGGGTTTCCGCCG 3305		6288 GCCAICCGAAGTIGGICCGGAGGCCTCGAIGGAGGAAGAAGAGCCCGGAGTCGT 6347	6228 CGATCAGACCGAGGACCCGGTTGGGCATGATGGGTTGGATCCAGTCCGGTC 6287	6168 TGTTGCCAGGTTCGGCCTTGGCCTGCACCAGACGTGCAATACGCCGTCGAACTCCGCA 6227	100 GANCCCTEATGANGTIGCTGCGGGTGGCCTGCAGGGGTCGGCGAGAGCTGGACGGGGTTGA 6167	3724 GGATCCGGCGCGCGTGCGGTGAGGTGAACTGGACGGGGGGGG	398 INTINCESTINGUTTINGUCANGANCIANGANCICTINGTINGANGANGICHACHA 6047	5928 CGAGGGTGAGCCACCTGCAGTTCGGGTGCTCGGGGGGTTCCTCGAAGACCTCGACCACCA 5987	5888 GLACGGAGGTCCATGTTCACCACGTTGTCGTAGCGAGCATCGCCCGCAGCTGGG 5927	Sava Gradic Griccata Recognic Code Code Control Code Code Code Code Code Code Code Code	5/48   GANCIGATISCICICICICICANGANGTANCICAGE/AGITICICGANGTANCICICTICGG	5080 GANGHARI LAGGIGGIGGIGGICGIGGICGIGGICGIGGIGGIGGIGGIG	1902   Telephole telepho		5508 GGGCGAGCATGCCGTGGTTGGCGGGGGGAGAGCAGCGGTTGCATCCAGGACCTCACCTCGC 5567

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CURRENT APPLICATION NUMBER: US/09/679,279
PRIOR APPLICATION NUMBER: US 60/158,305
PRIOR TILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 60/158,305
PRIOR APPLICATION NUMBER: US 60/190,024
PRIOR FILING DATE: 1090-03-17
NUMBER OF SEQ ID NOS: 34
SOPTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McDanie
                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (4651)...(5775)
LOCATION: (4651)...(5775)
OTHER INFORMATION: megDII,
OTHER INFORMATION: TDP-3-k
OTHER INFORMATION: SEQ ID 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic TITLE OF INVENTION: Genes and Uses Thereof FILE REFERENCE: 300622004700 CURRENT APPLICATION NATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: «
OTHER INFORMATION: S
NAME/KEY: CDS
LOCATION: (928)...(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (2072)...(3382)
OTHER INFORMATION: megDI,
OTHER INFORMATION: TDP-meg
OTHER INFORMATION: SEQ ID
                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (6592)...(7197)
OTHER INFORMATION: TDP-4-
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (5822)...(6595)
OTHER INFORMATION: megDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1)...(144)
                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (3462)...(4634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCACGGCGGGGAAAGGGCC 3109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTTGCTGCCGCCGGGC----GTTGTCGATCAAGACCCGCACTCACTGTAAGGGTCC 3130
                                                                                                                                                               (7220)
                                             (8228)...
                                                                                     ...(8206)
N: megDV, TDP-hexose 4-ketoreductase (eryBIV, dnmV
N: TDP-4-keto-6-deoxyhexose 4-ketoreductase;
N: SEQ ID NO NO: 9= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. (2061)
                                                                                                                                                                                                                                                                                                              megDIII, Qar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      megDVI, TDP-4-keto-6-deoxyglucose 3,4-isomerase, TDP-4-keto-6-deoxyhexose 3,4-isomerase; SEQ ID NO: 3= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                megDII, deoxysugar transaminase (eryCI, DnrJ homolog)
TDP-3-keto-6-deoxyhexose 3-aminotransaminase;
SEQ ID NO: 6= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           megDI, rhodosaminyl transferase (eryCIII homolog),
TDP-megosamine glycosyltransferase;
SEQ ID NO: 4= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           megBVI(megT), TDP-4-keto-6-deoxyglucose-2,3-dehydratase;
SEQ ID NO: 2= translated amino acid sequence
                                                                                                                                                                                                     megDIV, TDP-4-keto-6-deoxyglucose 3,5-epimerase TDP-4-keto-6-deoxyhexose 3,5-epimerase; SEQ ID NO: 8= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                megG(megY), mycarosyl acyltransferase, mycarose O-acyltransferas SEQ ID NO: 5= translated amino acid sequence
megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose 2,3-reductase;
SEQ ID NO: 10= translated amino acid sequence
                                             (9220)
                                                                                                                                                                                                                                                                                                                          daunosaminyl-N,N-dimethyltransferase (eryCVI homolog);
O: 7= translated amino acid sequence
                                                                                                                                                                                                                                                     (eryBVII, dnmU
                                                                                                                                     homolog),
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OTHER INFORMATION:
NAME/KEY: CDS
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LOCATION: (12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: (21517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_fe
LOCATION: (19876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc fe
LOCATION: (17155)
                       OTHER INFORMATION: megAII, KR4
                                             NAME/KEY: misc_feature
LOCATION: (32257)...(3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_fe
LOCATION: (22318)
                                                                                                                                                                                                                                                                                  NAME/KEY: misc_
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NAME/KEY: CDS
LOCATION: (22867)...(33555)
LOCATION: (22867)...(33555)
OTHER INFORMATION: megAII; SEQ II
NAME/KEY: misc feature
LOCATION: (22957)...(24237)
LOCATION: (22957)...(84237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (13576)...(13791)
OTHER INFORMATION: megAI, ACP-L
                     LOCATION: (29953)...(30477)
OTHER INFORMATION: megAII, DH4
NAME/KEY: misc_feature
LOCATION: (31396)...(32244)
                                                                                                                                                                                   LOCATION: (27393)...(28590)
OTHER INFORMATION: megAII, KS4
                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (27393)...(2)
                                                                                                                                                                                                                                            LOCATION: (26998)...(27258)
OTHER INFORMATION: megaII, ACP3
                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (26998)...(2)
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: megaII,
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (26230)...(2
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (24544)...(25581)
OTHER_INFORMATION: megAII, AT3
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (22957)...(24237)
OTHER INFORMATION: megAII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: megAI, ACP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (21517)...(22053)
OTHER INFORMATION: megAI, KR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (19876)...(20910)
OTHER INFORMATION: megAI, AT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (18268)...(19548)
OTHER INFORMATION: megal, KS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (17947)...(18207)
OTHER INFORMATION: megal, ACP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: megAI, KR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (15427)...(16476)
OTHER INFORMATION: megAI, AT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (13849)...(15126)
OTHER INFORMATION: megAI, KS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: megAI, AT-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (12505)...(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: megAI; SEQ ID
LOCATION: (31396)...(32244)
OTHER INFORMATION: megAII, ER4
                                                                                                                    LOCATION: (28897)...(29931)
OTHER INFORMATION: megAII, AT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (15427)...(1
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RMATION: megBIV, TDP-hexose 4-ketoreductase,

RMATION: TDP-4-keto-6-deoxyhexose 4-ketoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO: 12= translated amino acid sequence
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                                                                                                                                                                                                                                                                                                                                    (26733)
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                                                                                                                                                                                                                                                                                                                 (inactive)
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Qy 6475 GGGAGGTCCGCCGTGCCGAGTCAGGAAACGTATTGCCGATTGTGTGGATTCCGGAGTCGC 6534	Query Match 29.2%; Score 2606.8; DB 3; Length 47981; Best Local Similarity 99.9%; Pred. No. 0; Matches 2608; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 2608; CrcgArgcrcgGcgcgcgcgcgcgccAAccAgrcgrcgrcggrcggrggcGgr 6474  Qy 6415 CrcGAGCCGATGCTCGGCGGGCGGTGGGCCAACCAGTCGTGGACGTCGGTGGCGGT 6474	; OTHER INFORMATION: SEQ ID NO: 18= translated amino acid sequence; NAME/KEY: CDS ; NAME/KEY: CDS ; LOCATION: (46660)(47403) ; OTHER INFORMATION: megH, TEII; SEQ ID NO: 19= translated amino acid sequence ; NAME/KEY: CDS ; LOCATION: (47411)(47980) ; OTHER INFORMATION: megF, C-6 hydroxylase; SEQ ID NO: 20= translated amino acid seque US-09-679-279-1	INFORMATION: megGIII.2 (megBII), TDP-4-keto-6-c INFORMATION: megFIII.2 (megBII), TDP-4-keto-6-c INFORMATION: TDP-4-keto-6-deoxyglucose 2,3 de	; OTHER INFORMATION: megAIII, ACP6 ; NAME/KEY: misc_feature ; LOCATION: (42585)(43271) ; OTHER INFORMATION: megAIII, TE ; NAME/KEY: CDS ; LOCATION: (43268)(44344) ; OTHER INFORMATION: megCII, TDP-4-keto-6-deoxyglucose 3,4-isomerase; ; OTHER INFORMATION: SEQ ID NO: 16= translated amino acid sequence		; LOCATION: (37068)(37604) ; OTHER INFORMATION: megAIII, KR5 ; NAME/KEY: misc_feature ; LOCATION: (37860)(38120) ; OTHER INFORMATION: megAIII, ACP5 ; NAME/KEY: misc_feature ; LOCATION: (38187)(39470) ; OTHER INFORMATION: megAIII, KS6	LOCATION: (33052)(33312)  OTHER INFORMATION: megAII, ACP4  LAMB/KEY: CDS  LOCATION: (33666)(43271)  OTHER INFORMATION: megAIII; SEQ ID NO: 15= translated amino acid sequence  LOCATION: (33780)(35027)  OTHER INFORMATION: megAIII, KS5  NAME/KEY: misc_feature  LOCATION: (33785)(36419)  OTHER INFORMATION: megAIII, AT5  NAME/KEY: misc_feature
Db 1141 GCCGAGGTGCCCGATCCGGGCTTCACCCACGGCCGAGGTTCTACGCCGGTGGATG 720  Qy 7615 CAGGTGGCCCACTGCCCGGCGGCGCTCCTGGGCCGGCGAGGTTCTACGCCGG 7674		Qy 7315 TCACAGTCTTCAATCCGGAGGGTTCTATGGCAGTTGGCAAGGCGGCTGGGCCGG 7374	Qy 7195 GGAAATCCGTGCCACCGGTCGTCCGCAGTGACGACGACCGGGTTTCGAGACAGCA 7254	Qy 7075 GGAAGGGTGGCGGATCAGGGAAATGGCCGTGTCACTAGACAGAC	Oy 6955 CATGGTCCGCCGGGGGGTCCGACAGGCCCGAAACGCCCGGCATCCAGCCTGTTCGACGA 7014	Qy 6835 GACCGGTTGCGGCGGTTTTTCGCCCGTTTCCGAACTGCGGATTCGTCGATCGCGCAGGTG 6894	Qy 6655 CGGGAGAAGGTCCGTCGAACAACTTCCGGGTGAACCGGTCGACGGCGTCGAACGGGC 6714  Db :::// 241 CGGGAGAAAGGTCCGTCGAACAACTTCCGGGTGAACCGGCCGG

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 TCGGACAACCTGCCGTCGTCCCGACCGCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGC
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APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Liu, H.

APPLICANT: Zhao, L.

ITILE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 13613

TYPE: DNA

ORGANISM: Streptomyces venezuelae

US-09-105-537-3
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US-09-105-537-3
; Sequence 3, Application
; Patent No. 6265202
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Best Local Similarity 67.7%;

Matches 1850; Conservative
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Pred. No. 7.2e-206;
0; Mismatches 876;
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TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-06-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER: 60/100,880
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Best Local Similarity 68.1%;
Matches 1015; Conservative
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TYPE: DNA
ORGANISM: Streptomyces venezuelae
;-09-320-878-24
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APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, ROBERT
APPLICANT: TANG, Li
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APPLICANT: ABTLACH, Melanie C.

APPLICANT: BETLACH, Melanie C.

APPLICANT: BETLACH, Mary

APPLICANT: BETLACH, Mary

APPLICANT: EBTLACH, Mary

APPLICANT: TANG, Li

TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Usin

TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold

FILE REFERENCE: 300622002100

CURRENT APPLICATION NUMBER: US/09/141,908

CURRENT FILING DATE: 1998-08-28

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER APPLICATION NUMBER: PCOV. 60/076,919

EARLIER FILING DATE: 1997-04-30

EARLIER FILING DATE: 1998-03-05

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1998-05-28

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; SEQ ID NO 22
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; TYPE: DIA
; ORGANISM: Streptomyces v
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; Sequence 24, Application US/09657440
; Sequence 24, Application US/09657440
; Patent No. 6509455
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE

RESULT 6

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FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
FRIOR APPLICATION NUMBER: 09/320,878
PRIOR PILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 24
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; ORGANISM: Streptomyces
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US-09-793-708-24/c

US-09-793-708-24/c

; Sequence 24, Application US/09793708
; Parent No. 6902913
; GENERAL INFORMATION:
 APPLICANT: ASHLEY, GARY
 APPLICANT: BETLACH, Melanie C.
 APPLICANT: MITCHACH, Mary C.
 APPLICANT: MCDANIEL, ROBETL
; APPLICANT: MCDANIEL, ROBETL
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE
TITLE OF INTENION NUMBER: US/09/793,708
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 09/657,440
; PRIOR FILING DATE: 1990-05-27
; PRIOR APPLICATION NUMBER: US 09/141,908
; PRIOR APPLICATION NUMBER: US 09/141,908
; PRIOR APPLICATION NUMBER: US 09/141,908
; PRIOR APPLICATION NUMBER: US 09/073,538
; PRIOR APPLICATION NUMBER: US 09/073,538
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/073,538

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Best Local Similarity 68.1%;
Matches 1015; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 1565
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                        TAGACGGTGGGCCGCAGGCCGTGGTGGCGTGCGCGGCCAGGCTCCCGAGGCCGGG
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Pred. No. 7.5e-111;
0; Mismatches 476;
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                                                                                                           AGCCGGACGAGGTGGCGGGCGGTCGTTCCGGCCTCGTCGGCGCACGAGGCCGCCGCCG
                                                                                                                                     AGTTCGGCGAGCCGGACCGCCTGTCGTTCGGCGGCGTGTCGGATGCCGGCACCGGTGAGGCGG 3748
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Sequence 9, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
CURRENT APPLICATION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1458
TYPE: DNA
CURGANISM: Streptomyces venezuelae
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US-09-105-537-9/c
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Best Local Similarity
Matches 980; Conserv
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                    CCGGGCGGTCACCGACTGGTCGAAACCGTCGAGAAGAACTCGTCCCCCGGCTGCGGATC
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ilarity 69.5%;
Conservative
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Pred. No. 1.2e-109;
0; Mismatches 430;
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                                                                                                                       Query Match
Best Local Similarity
Matches 1118; Conserv
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3756 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED
TITLE OF INVENTION: BIOSYNTHESIS GENES
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                   NAME: Dianne Casuto REGISTRATION NUMBER: P-40,9 REGISTRATION NUMBER: 58 REFERENCE/DOCKET NUMBER: 58 TELECOMMUNICATION INFORMATION: TELEPHONE: (847) 938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Abbott
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                           STRANDEDNESS: Sir
                                                                                                                                                                                                                                               TYPE: nucleic acid
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CGGGGTCTCTACTGGGGGTTCGGTGCCAACGGCGATCTGTACTCGATGCTCCTGTCCGGA
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                                                                                                                       Score 701.4; DB 2;
Pred. No. 3.2e-106;
0; Mismatches 526;
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              CTCTGAGGATTCCGCGATGCGCGTCGTCTTCTCCTCCATGGCCAGCAAGAGCCACCTCTT
                                            CTGTAGAGGAAGAACGATGCGCGTCGTGTTTTTCATCGATGGCTGTCAACAGCCATCTGTT
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APPLICANT: Liu, H.

APPLICANT: Xue, Y.

APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 7

LENGTH: 1248

TYPE: DNA

ORGANISM: Streptomyces venezuelae

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                                                                                                                                                                                                                                                                                                Query Match 6.7%;
Best Local Similarity 69.2%;
Matches 812; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application Patent No. 6265202 GENERAL INFORMATION:
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                                                                                                                                                                                                                                              3926 CGCGTTGATCAACGCACCGCTGGTGGTGGCGAGTCGGATGACGTCGCACACCCCGGCGGAT
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 21
LENGTH: 5970
TYPE: DNA
ORGANISM: Streptomyces vons-09-320-878-21
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Patent No. 6
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Best Local Similarity 70.1%;
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APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary C.
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          GCTGGTCGGCCCCACAGGTGTACGCCGACGATCGCGCCGGTCTGCGGGGTGACGAGCGCG
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Pred. No. 2.5e-76;
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TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold : FILE REFERENCE: 300622002100 : CURRENT APPLICATION NUMBER: US/09/141,908 : CURRENT FILING DATE: 1998-08-28 : EARLIER APPLICATION NUMBER: CIP OF 09/073,538 : EARLIER FILING DATE: 1998-05-06 : EARLIER FILING DATE: 1998-05-06 : EARLIER FILING DATE: 1997-04-30 : EARLIER FILING DATE: 1997-04-30 : EARLIER APPLICATION NUMBER: EROV. 60/076,919 : EARLIER APPLICATION NUMBER: PROV. 60/076,919 : EARLIER APPLICATION NUMBER: PROV. 60/087,080 : EARLIER FILING DATE: 1998-03-05 : EARLIER FILING DATE: 1998-05-28 : NUMBER OF SEQ ID NOS: 31
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Best Local S
Matches 698
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APPLICANT: BETLACH, Melanie C
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
APPLICANT: TANG, Li
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 4164 CGGTCGATGCCGGTGGCGGTGCCGTCCACCAGGATGATCACGTACTGGTAGTTGCTCTCC
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                                                                                  Sequence 21, Application US/09657440 Patent No. 6509455
GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
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CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
LENGTH: 5970
TYPE: DNA
ORGANISM: Streptomyces venezuelae
US-09-657-440-21
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 09/657,440
PRIOR FILING DATE: 2000-09-07
PRIOR PRIOR APPLICATION NUMBER: US 09/320,878
PRIOR PRIOR DATE: 1999-05-27
PRIOR APPLICATION NUMBER: US 09/141,908
PRIOR FILING DATE: 1998-08-28
PRIOR PRILING DATE: 1998-08-28
PRIOR PRILING DATE: 1998-05-06
PRIOR PRILING DATE: 1998-05-06
PRIOR PRILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/846,247
PRIOR PRIOR PRIOR DATE: 1997-04-30
PRIOR PRIOR PRIOR DATE: 1999-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
SERGIH: 5970
TYPE: DNA
ORGANISM: Streptomyces venezuelae
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Best Local Similarity
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APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE
FILE REFERENCE: 300622002121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ASHLEY, Gary APPLICANT: BETLACH, Me
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                       4284 AGCGCGTGGTTGACCCGGTTGTGCTCCCTGGTCTCGGCGAACGCTCGAGGGAAGGTGAGC 4343
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BETLACH, Mary C.
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Sequence 30, Application US/09758759
Patent No. 6861513
GENERAL INFORMATION:
APPLICANT: Hosted, Thomas J.
APPLICANT: Wang, Tim X.
APPLICANT: Wang, Tim X.
APPLICANT: Horan, Ann C.
TITLE OF INVENTION: Everninomicin Biosynthetic Ge.
FILL REFERENCE: 100983K US
CURRENT APPLICATION NUMBER: US/09/758,759
CURRENT APPLICATION NUMBER: US/09/758,759
CURRENT PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: US 60/175,751
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 204
SEC ID NOS: 204
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US-09-758-759-30/c
       SEQ ID NO 30
LENGTH: 1452
TYPE: DNA
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; LOCATION: (1)..(145
; OTHER INFORMATION:
US-09-758-759-30
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Matches 820; Conserva
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                                                                             GCTCGGGCGGGTCCTCGAAGACCTCGACCACCATGTTGCGGTTTGCGGTTTTGCGCAGGAACCC
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Adn97589 S ambofac	2 ADN97589	H	1410	5.0	451.2	45	ი
Adm80073 Spiramyci	2 ADM80073	H	1410	5.0	451.2	44	ი
Aas08693 Micromono	AAS08693	տ	109519	5.2	461.2	43	
Abz66810 Orthosomy	0 ABZ66810	10	37116	5.2	461.2	42	a
Abz66691 Orthosomy	0 ABZ66691	ij	1455	5.2	461.2	41	ი
Adn97550 S ambofac	2 ADN97550	12	30943	5.2	463.4	40	a
Adm80034 Spiramyci	2 ADM80034	H	30943	5.2	463.4	39	ი
Aea48864 Angolamyc	4 AEA48864	14	4461	5.3	471.2	38	
Abz37515 Streptomy	ABZ37515	8	59816	5.3	474.2	37	ი
Abz37516 Streptomy	ABZ37516	8	59816	5.3	474.2	36	
Abz37564 Streptomy	ABZ37564		1404	5.3	474.2	35	ი
Abz66689 Orthosomy	0 ABZ66689	10	1401	5.6	496.6	34	ი
Abz66808 Orthosomy	0 ABZ66808		45055	5.6	500.4	ü	ი
Abs56092 Contig 00	0 ABS56092		5970	5.8	519.2	32	
Adh53464 S. venezu	0 ADH53464	10	5970	5. 8	519.2	31	
Ada09420 S. venezu	ADA09420	œ	5970	5.8	519.2	30	
Aaz56003 Contig 00	AAZ56003		5970	5.8	519.2	29	
Aaa75635 Nucleotid	Þ		5970	5.8	519.2	28	
Adl91935 Streptomy	2 ADL91935	12	1248	6.7	595.4	27	Ω
Aad39044 Streptomy	AAD39044		1248	6.7	595.4	26	ი
Aaz87286 S. venezu	AAZ87286	w	1248	6.7	595.4	25	Ω
Aad55827 Micromono			1227	6.7	596.6	24	ი
Adil4148 M. megalo	2 ADI14148		17596	6.9	612.8	23	
Aad55828 Micromono	0 AAD55828		1467	7.5	667.2	22	Ω
Aat72684 Sugar bio	AAT72684	N	3756	7.8	701.4	21	
Aax25772 S.erythra	AAX25772	N	3412	8.0	711.6	20.	ი

## ALIGNMENTS

RESULT 1 ADI14147 ID ADI1 15-APR-2004 (first entry) ADI14147; ADI14147 standard; DNA; 9024 BP.

ds; polyketide; enzyme; MegR; MegR; MegK; MegCIV; MegBVI; MegBIII; MegL; MegM; megosamine; megalomicin.

M. megalomicea cosmid pKOS079-138B SEQ ID NO:1.

Micromonospora megalomicea.

WO2004003169-A2.

08-JAN-2004.

30-JUN-2003; 2003WO-US020681

28-JUN-2002; 2002US-0393016P

(KOSA-) KOSAN BIOSCIENCES INC

Hutchinson RC, Katz L, Reid R, Hu 7 Gramajo H;

WPI; 2004-203379/19.

Novel isolated, purified, or recombinant nucleic acid comprising polyketide modifying gene, there gene encodes polyketide modifying enzyme e.g., MegR, MegK, or MegM enzymes useful for producing modified polyketide.

Example 2; SEQ ID NO 1; 51pp; English.

The invention relates to a novel isolated, purified, or recombinant nucleic acid (I) comprising a polyketide modifying gene, where the gene encodes a polyketide modifying enzyme chosen from MegR, MegR, MegK, MegK, MegCV, MegCV, MegCV, MegBIII, MegL, and MegM enzymes. A method of the invention is useful for producing a modified polyketide, which involves culturing a recombinant cell comprising the recombinant nucleic acid

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                                                                                                                                                                               GTCACGATCGTCGCCGAGCTGCTGGGGCTGCCCCGGATGGACCACAAGCAGTTCGGTGAC
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                   GAGATCCCGGCCGACGTCATGGTCAACACCTGGGTGCTCTCGGCCAACCGCGATCCCCTG
                                         ACGGCCGCCGAGGACCCGGGTCTGATCGCGCCGATCATCGAGGAGGTGTTTCCGTTTC
                                                                                                           ACCACCACCGTCCTGCTGGGCAACATCGTCCGCACCCTCGACGAGCACCCCGGAGTACTGG
                                                                                                                                             ACCTTCGACGACGTGGAGGCGGCCAACTTCTCCACAGCGTTGCTGCTGGCGGGGGACATC
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4141 GCAGGATCGCCTGCAGCCGGTCACGGTCGATGCCGGTGGCGGTGCCGTCCACCAGGATGA 4200	061 CCTGACCCGTTCGAAGGCGCCACGCTTGCCGGTGGTGGCCTGGTACTCGTCGTTGTTCAG
4081 AGGGCGTCATCTGGTGGCAGGCGGGGAGAAGTAGGGCTGTGCGACGACCTTCTCCGCGC 4140	3001 GCCGAGCCGGAGCCGGTCGGCCGCTCGGCAGCATCCGCAGGAAGTCCCGGAGGTTCTT 3060
4021 CGAGCACCCGTTCGGCGACCCACTCGGTCTGTGTCAGCCGCAGCGGTGGCTCCGTGCGGT 4080	2941 GATGAAGTCGACCAGGTCGATGAGGCGGTTGGCCCCGGCAGGATGATGTTGGTTG
GATGACGTCGCACACCCGGCGGATGTCCTCACTGGACACCCGAGGGCCGGTCGGAGGG	2881 GTCCTCGCGGACGGTGACGAAGTCGAGCGGCCGGTGCGGGCTGGACTCGTTGAGTTCGGC 2940
01 CGTTGCGTTTGCCCTTGTCCCACTCCGCGTTGATCAACGCACCGCTGGTCGTGGCGAGTC	2821 GCCTCCCGCAACTCGGTCCGTTCGCCCTCGGACACCTGCCGTCCGACCGA
3841 AGAGTGGTCTTCATCGACGTGCGAACCCTTCTGGCGTTCGTGGTGCGAGGATCACGAAC 3900 	2761 ACCCAGGTCGGTCTGCATGCCCGGGGTCCGCCTCGGCGGTAGTCGACCGAGCGAG
781 781	2701 TTCCGGCCGGATCCGCAACAGCTGGGCGTCGACACCCCGACGCAGGCTCTCCAACGCGTA 2760
3721 GETGTCGGATGCGGCACCGGTGAGGCGGTGACCTCGGCGCTGAGCGCCCGCACCACGGC 3780	2641 GACGTCTCCGAGCAGGTCGATCTGCACCGCCACCTGCGGATGGGCGGTCGGGCGCATCGT 2700
3661 GAACGGCAAGGCCCGTAATGGGCGATGAATTCGGCGAACCGGACCGCCTGTCGTTCGGC 3720	2581 GCCGGCGACGTAGCGGGTGGCCCCGGCCAGCCCGGGGAAAACCGGCCTCCCGGTACAGGTA 2640
601 CAGCTCGCCGAACCCGGTCCAGGTCGAACCGACGCCATCTGCTCCAACGGGGT [	Qy         2521         GCGGCCCGACGTGACGAAGTCGTGGACGACCGACGGACGACCGAGGTCCCGGGTCCCGGGGTGACCCG         2580           Db         2521         GCGGCCCGACGTGACGAAGTCGTGGACGACCGAGTGCAGGCTCCGGGTCCGGGTGACCCG         2580
GCCCGCCGGGCCCTGCTCCACCGCCGTGCCCAGCTGCGGATCGAACAGGTTCGAG 	Qy         2461         GGTCACCGACTGGTCGAAACCGTCGAGGAAGAACTCGTCCCCCGGCTGCGGATCGATGCT         2520         Db         Db         Db         CAGTCACCGACTGGTCGAAGCAACCGTCGAGGAAGAACTCGTCCCCCGGGTGCGGATCGATGCT         Db         Db         CAGTCACCGACTGGTCGAAGCACCGTCGAGGAAGAACTCGTCCCCCGGGTGCGGATCGATGCT         2520         CAGTCACCGACTGGTCGAAGCAACCGTCGAGGAACTCGTCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGGAACTCGTCCCCCGGGCTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGGAAGAACTCGTCCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGGAAGAACTCGTCCCCCCGGGCTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAGCAACCGTCGAAGGAACTCGTCCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGGAACTCGTCCCCCCGGGCTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGGAACTCGTCCCCCCGGGCTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGGAACTCGTCCCCCCGGGCTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAGAACCTCGTCGAAGGAACTCGTCCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGAACTCGTCGCCCCCGGGCTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCGTCGAAGAACTCGTCGCCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAACCTCGTCGAAGAACTCGTCGCCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAGAACTCGTCGAAGAACTCGTCGCCCCCCCGGGTTGCGGATCGATGCT         CAGTCACCGACTGGTCGAAGAACTCGTCGAAGAACTCGTCGAAGAACTCGTCGCCCCCCCGGGTTGCGGATGCT         CAGTCACCGACTGGTCGAAGAACTCGTCGAAGAACTCGTCGCCCCCCCC
TACCGCAGCCTCCAACGCCGCCGGCGGCGTTCAGCGGGCCTGATCGTGTTGGTCCAGTACTT	2401 CAGGCCCGATGCTGATCCCACCCGTCGGCGACGTCCCGTTCGAGTTGGTTG
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3121 CCCGTACAGGAGGTACGGACCGCGCGAGGTCCCACAGGCCGGGCTGGCGGCGACGT 	Qy         2041         TCCTTCGGGCACGCGTGCACTTCTGTCTCGGTGCCCCGCTGGCGCGCCCTGGAGAACCAG         2100         Db         Db         2041         TCCTTCGGGCACGGCGTGCACTTCTGTCTCGGTGCCCCGCTGGAGAACCAG         2100         Db
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6301 GGTCCGGACGTGCAGGCCCTCGATGGAGAAGAAGCGCCCGGAGTCGTGCGCCAGCCGACC	un un	221	용 원
	GAAGGTCATCCACCGGTGGTCGGG 5220	5161 GTAGTGGCTGTGCGCGAGCAGTTCGGTGATCTGGCCGAAGGTCATCCACCGGTGGTCGGG	유 원
	GAGGCTGCGCAGCTGGATGTTGAC 5160	5101 CGTCGCCCGGTTGTAGACGGCGGACGCGACGCGACGCGA	유성
	ARTCGGTCGGTACGCGCTTCACGC 5100	5041 GGTGCAGGAACGCCTCGGGACCGCCGAAGATCGCCAGATCGGTCGG	음 성
61	rcgrcggccggccacgrgcaggg 5040	4981 ACTCCAGGCGGGCCAGGAACCGCTGCCGGTCGCCGATCGTCGGCCGGC	유 성
	TGAGCCAGTTGTTGTTCAGGGCCC 4980	4921 GGGCCTCGAACTCCCGCACCAGGGGCCCGCTGGTGAGCCAGTTGTTGTTCAGGGCCC	용 왕
2 4 2	FTACCCCGACCAGGTCGGCGACCC 4920	4861 GGGCGACGGTGGCGTTGCAGGTGGCGATGCAGTGCCGTACCCCGACCAGGTCGGCGACCCCGACCAGGTCGGCGACCCCGACCAGGTCGGCGACCCCGACCAGGTCGGCGACCCCGACCAGGTCGGCGACCAGGTCGGCGACCAGGTCGGCGACCAGGTCGGCGACCAGGTCGGCGACCAGGTGCAGGTGCAGTGCAGTGCAGTGCAGTACCCCCGACCAGGTCGGCGACCA	음 성
81	ACCGGCCCGCAGCACCAGTTCCA 4860	4801 AGGTCATTGACGGCATGATCACTTCACCGGTGACGTCACCGGCCGCAGCACCAGTTCCA	음 성
21 2	rcaccacaracacaaraaccacaa 4800	4741 CGACGTCGCAGAACACCGGTGTGAGTCCGAGCCAGCTCGCCGCGTGCGCGGTGGCCGCGAGACACCTCGCCGCGTGCGCGGTGGCCGCGAGACACCGCGAGCCAGCC	음 성
761	GTCGACCAGACCGGTCGCCGGGT 4740	4681 CGGTCTGCGGGGTGACGAGCGCGGCGACGTGGTCCGGGTCGACCAGACCGGTCGCCGGGT	용 성
2 2 2	ACAGGTGTACGCCGACGATCGCGC 4680	4621 TCTTCGCCAGCGCCTCCACAGGTGCTGGTCGGCCCACAGGTGTACGCCGACGATCGGCGC	용 성
4 1	CTTGACCTGGTGGTCGGCGGCGA 4620	4561 TCGTGCAGCCCAGGGCGTGGGCGGCGTCGAAGAAGAGCTTGACCTGGTGGTCGGCGGCGACGACGACGACGACGACGACGACGACGACGAC	용 성
581	TCCGCCCACCGACGTCCACCCG 4560	4501 TGGTGGCGTGGAAGCTGAACACCTCGGCGTCACCGGATCCGCCCACCGGACGTCCACCCG	용 성
י בי	COCCTCGAAGGCGGTGACCGCCT 4500	4441 GTTCGGCCAGCAGCCGTCGTCGGTGACCACCGCCCCCCCC	유 성
	CRAAGITGIGCATGGCCCGGATCC 4440	4381 TGCCGATCTCGGTGACCACCTTGTCCGGGCCGAAGTTGCCGAAGTTGTGCCCGGATCC	음 성
	GCACTCGCTCATCTTGCCGTTGG 4380	4321 CGAACGCGTCGAGGGAGGTGAGCCCCATGGCCGCGGCGCACTCGCTCATCTTGCCGTTGG	음 성
41	CCGGTTGTGCTCCCTGGTCTCGG 4320	4261 CGTCGCGCAGCTCGCTGGTGTAGAGCGCGTGGTTGACCCCGGTTGTGCTCCCTGGTCTCGG	유 성
81	4260 4260	4201 TCACGTACTGGTAGTTGCTCCTCGTCGGGCGGGAGCGAGTGCACGGTGACGCCGGGTA	음 성
5281 GTAGAACCGCCCACCCTCCTCGGAGTY	GGCGGTGCCGTCCACCAGGATGA 4200	4141 GCAGGATCGCCTGCAGCCGGTCACGGTCGATGCCGGTGGCGGTGCCGTCCACCAGGATGA 4200	뮹

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8521 CCATCTGTTCGGGCTGGTCCCGCTCGCAAGCGCCTTCCAGGCGGCCGGACACGAAGGTACG 8580	ig 7500   Qy	7441 CTGTCCGGACGGGACGACGACCCCTGGACCTGGTACGAACGGTTGCGGGCCGGACGG
8461 CCGGTCGAGCTGTAGAGGAAGGAACGATGCGCGTCGTGTTTTCATCGATGGCTGTCAACAG 8520		7381 CAGATGGCCCGGGGTCTCTACTGGGGGTTCGGTGCCAACGGCGATCTGTACTCGATGCTC
8401 CGTTCCGGGCCGGTGATCAGACGACGTCGGTCACCCGTCGCCCGTGGTCTCAGCCGTTGC 8460		
8341 GTGGCCACCCTGGCCACGGCGGCGCTGCGGGCCGCCGGCTGTTGCCCCGGCTGTCC 8400		7261 AGGCGATGCAGGCGTTTCGTCTCGCGCCCGGACGCGTCGCACTAGGTGGAATCCGTCACAG
8281 GGCGACGCCGAGATCCTGTCGTCCCGGCCCGGCTCGCCCCGCACCGACCCTCGACGCCCTG 8340		
8221 GCGGCGAACCGTGATCCCGAGGTCTTCACCGATCCCGATCCGGTTCGACGTGGACCGTGGC 8280		7141 GCGGAAACAGCATCGACCGTCAGCCGTTCATTGCCCCCGGCGGCACCGCCTTGGAAAT
8161 GACCGCCGGGTGGGCGGGGTCGACGTCCCGACCGGTGGCGACGTGACAGTGGTCGTCGCC 8220		7081 GTGGCGCGATCAGGGAAATGGCCGTGTCACTAGACAGACGCCAAACAGCTGTCCGGGCCT 
8101 GTGACGGAGGTGTCGCGGACGAGTCCCGGCGTCCACCTGGAACGCCGCACCGCGCGCG		7021 CATCACCGTGCAAGCCGCGATGACACCACGCCATGCTGGTGCCGCACTGGAAGG
8041 ACCGAGCTTCCCGAACTGGCGGCACGACTTGCCGACGACCCGGAGACCCGGACCCGGTGTG 8100		6961 CCGCCCGAGGGTCCGACAGGCCCGAAAACGCCCGGCATCCAGCCTGTTCGACGACGTCGA
7981 CTGGTGGGGGTGGTGGCGAACTGGCGAACACGGTGGGCAACGCCGTCCTGGCCGTC 8040	917 6960 Qy 	6901 GGTGGCTGACCGGGATGATCTGCAATCATGGCGCTCAATGACGATCTCTTGTAGCATGGT 
7921 CAGGCGCTGACCGCCCTCGACGAGATCGACGCGGTCACCGGCGGTCGGGACGCCGCGGTG 7980	6900	6841 TTGCGGCGTGTTTTCGCCCGTTTCCGAACTGCGGATTCGTCGATCGCGCAGGTGGGAGCG
7861 TCGGCGACCCGGGTATGCCTGGACGCCCAGGTCAGCCCGCAACAGCTCGCGGTGACCGAA 7920	3G 6840 Qy 	6781 GTGTGTTCCGTGGTATGACGCGTTCCCGGCCCGTCTGGAACTGTGCGTGGGACTGACCGG
7801 GCGCTCGGTACCGCGCCCGCACTCAAGGGCGTGGACCCCGACCGTCTCCGGTCCTGGACC 7860	2G 6780 QY 	6721 GCACCCGATCATTGCTGTCGGTGAACTTCCTAACTGTCGGCGCGCACATCTTTCTGACCG
7741 ACCGAGCTGGGGTCGCGCTTCGATCTCGTGAACGACTTCGCCCGGGAGGTCCCGGTGCTG 7800	A 6720 QY   Db	6661 AAGGTCCGTCGAACAACTTCCGGGTGACCGGTCGCCGGCGTCGACAACGGCCGTCGGA
7681 GACGCGGCTCGGTGACACTGGACGCCGACTGGCTCCAGCACCGGTCCGCCCAGGCTGGTG 7740	Qy 1G 6660 Db	6601 CCGGACTGACATTCGTCGATCAAGACCCCGCCCAGTGTAGGGCTCCGCCCCGCGACGGGAG
GCCACTGCCGGGGGCCTCCTGGGCCGGCCCCTTCCGGGAGTTCTACGCCCGCACCGAG	6600	6541 GTTGACCCGATCCCCCATACGCCTCTCCCGTGATGTCGTGGGCGGTCCGTGCGGTACCGC
7561 GTGCTCGCCGATCCCGGCCTTCACCCACGGCCCCGACGCTGCCCCGCTGGATGCAGGTG 7620	CC 6540 OY	6481 TCCGCCGTGCCGAGTCAGGAAACGTATTGCCGATTGTGTGGATTCCGGAGTCGCATGACC
GAACCGTAACGCCAATCGGGCCGGAACGTGGGTGGTCGGTGACCACCGGACCGCCGCAGGGACCGTGAGCGACCGCAGTGGGTGG	6480	6421 CCGATGCTCGGCGGCGGTGGGCCAACCAGTCGTGGACGTCGGTGGCGGTGGGAGG
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/gene= "eryBVI"
/product= "dTDP-
4837. .6042
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1210. .2457
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                                                                                                                                                                                                                                                                                                                                        'label= ORF13
                                                        'label= ORF16
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                     "dTDP-4-keto-L-6-deoxyhexose-2,3-dehydratase"
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     GGTTGAGCCGGGCGGTCACCGACTGGTCGAAACCGTCGAGGAAGAACTCGTCCCCCGGCT
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WPI; 1999-142938/12
                                         Fromentin C,
Gaisser S,
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12-JUN-1998;
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                                                                                     (HMRI ) HOECHST MARION
AAW99389, AAW99390, AAW99391,
                                          Leadlay
                                          Michel J,
Leadlay P, |
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98FR-00007411.
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/label= ORF19
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/product= "dTDP-D-4,6-dideoxyhexose-3,4-reductase"
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product= "dTDP-D-6-deoxyhexose-3,4-dehydratase"
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label= ORF18
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                                          Raynal M,
Mendez C,
                                            Salah-Bey K,
Salas JA;
 AAW99392,
   AAW99393, AAW99394,
                                                           Cortes
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New nucleic acid sequences encoding enzymes involved in macrolide biosynthesis - useful for producing hybrid secondary metabolites, particularly erythromycin analogues.

Claim 8; Fig 3; 221pp; French.

This sequence represents the eryAI-eryK gene cluster from the Grampositive bacterium Saccharopolyspora erythraea which encodes enzymes involved in the production of the macrolide antibiotic erythromycin as a secondary metabolite. The erythromycin gene cluster spans approximately Sakb and contains at least 20 open reading frames (ORF). This sequence contains the eryBIV, eryBV, eryCVI, eryBVI, eryCVIV, eryCVV and eryBVII genes encoding ORFs 13, 14, 15, 16, 17, 18 and 19 respectively. A DNA representing the eryG-eryAIII region of the same cluster is shown in AAX25772. The genes are used to produce hybrid secondary metabolites in S.erythraea, i.e. erythromycin analogues which may have improved properties or as hybridisation probes for isolating homologous genes involved in glycosylation of macrolactones in macrolide-producing strains especifically oleandomycin-producing strains of Streptomyces antibioticus)

Sequence 8160 BP; 1259 A; 2927 C; 2789 G; 1185 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 3532; Conserv AGACGGCGCGATCAGGCCCCGATGCTGATCCCACCGTCGGCGACGTCCCGTTCGAGTT GTCGGGGGTGAACTCGAAACCGCCCGCCACCGCCAGCTCACGTACTCGCAACTCCGGTTC Conservative 34.0%; 80.3%; Score 3037.4; Pred. No. 0; 0; Mismatches 0; 863; DB 2; Indels Length 8160; 6 Gaps 7548 7608 2327 2447 2387 2507 7488 N

2567 2567 2567 27368 7368 7368 7308 7308 7308 7308 73248 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Db 6467 CAGGCTTGCGGTAGACCGCCGCGTCCAGTGCGCCTGCGGCGTCCAGCGGCTTGATCGTGT  Oy 3528 TGCTCCAGTACTTGCCCGCCGGGCCCTGCTCCACCGCCGTGCCCAGCTGCGGGATGCGAT		Qy 3408 AGAAGTGACAGCGGAACATGCACGTCGGGCCGGGGTAGAGCCCGACGCTGTACGGGAAGG	QY 3348 GGATCTCGTTGCCGGGCACCACCGCGTCGTACTTGGCACCCGTACGCGTACG	6647	3288		3228	Qy 3168 GGCGGCAGCGTCTGTTCGGTGAGGGCGAAGGCGTTGGTGAGACGGTCAGGGCGAAG	OY 3108 CGTCGTTGTTCAGCCCGTACAGGGAGGTACGGACCGCCGCCGAGGGCCCACAGGCCGGGCT	6887	Db 6947 TGATGTGGTTGAAGCCGAGCCGGATCGGCGCTCCGCTCGGCGCATCGCATCGATCG	2988	Qy 2928 CGTTGAGTTCGGCGATGAAGTCGACCAGGTCGATGAGGCGGTTGGGCCGGCC	Qy 2868 CCCGACCGCTGTAGTCCTCGCGGACGGTGAAGTCGAAGCGGCCGGTGGGGCTGGACT	Db 7127 CGAACCGCACCAGGCCCTCGCGCAGCTCGTTGCGCTCGGAGTCCGACAGCCGGCCG	7187	QY 2748 TCTCCAACGCGTAACCCAGGTCGGTCTGCATGCCCGGGGTCCGCCTCGGCGTAGTCGA	QY 2688 TCGGGCGCATCGTTTCCGGCCGGATCCGCAACAGCTGGGGCGTCGACACCCCCGACGCAAGGC	7307	2628	QY 2568 CCGGGGTGACCCGGCCGGCGACGTAGCGGGGTGGCCCCGCCAGCCCGGGGAAACCGGCCT	7427	Qy 2508 GCGGATCGATGCTGCGGCCCGACGTGACGAAGTCGT
8 4 4 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	3587 Oy	GT 3527	3467 Db	C 3407 Db	6588 Db	3347 QY	3287 Db	3287 Qy	C 3227 Db	3167 Db	Db	GGAAGC 6888  GGAAGC 6988  Qy	3047 Qy	2987 Db	2927 Db	2867 pb	A 7128 OY	2807 Oy	2747	7248 Db	2687 Qy	2627 Db	7368 Db	Q

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                                                                         CCGCCTCGGTGCGCAGGTGCACGAGCGCGTGGAGGGTGCCGTCGATCTCCTTGACCAGGA
                                                                                                                      CGGTGTAGTTGTCCGGCTGACAGTGCACCGTCGCCGCCAACTCGGCGACGTCGTGGCCAC
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Best Local Sin
Matches 3529;
                                                                                                                                             2 Polynucleotides (AAT72684 and AAT72685) represent 2 distinct clust of genes encoding enzymes (AAW19734-36 and AAW19737-42) involved in biosynthesis and attachment in Saccharopolyspora erythraea. The eryB genes are involved in the biosynthesis of I-mycarose and the eryC ge involved in the biosynthesis of D-desosamine. Novel glycosylation—modified polyketides are produced by selectively altering, inactivat or augmenting these eryB and/or eryC genes and introducing them into
                                                                                                                                                                                                                                                        generate poly:
glycosylation.
                                                                                                                                                                                                                                                                  New genes involved in sugar biosynthesis and attachment generate poly:ketide antimicrobials etc. with altered page 1.
                                                                                                                                      polyketide-producing
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                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1995;
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8051
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                                                      Katz
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5917. .7
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/label= eryBV
2348. .3061
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/label=
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7415. .7996
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1048. .2295
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3214. .4677
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Pred. No. 0;
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                                                                                             CGCCGGAGAGGTACATCGCCGTCGGGTTCTCCGACGGCACCTCGTCGATGACCGAGGTGA
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                                                                                                                                              CCGCTTGCTGCCGCCGGGC----GTTGTCGATCAAGACCCGCACTCACTGTAAGGGTCC
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AAF30757 standard; DNA; 47
XC AAF30757 standard; DNA; 47
AC AAF30757;
XX AAF30757;
XX Micromonospora megalomicae
XW Megalomicin; meg gene; pol
XW Antiparasitic; ds.

OS Micromonospora megalomice;
XX Micromonospora megalomica;
XX Micromonospora me
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                                                                                                                   /gene= "megBV"
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/note= "encodes AAB82210"
/complement(10483, ..11424)
    /gene "megBIV"
/product= "TDP-4-keto-6-deoxyhexose
/product= "encodes AAB82211"
12181. .22821
/*tag= 1
                                                                                                                                                                                                  complement (9226. .10479)
/*tag= j
                                                                                                                                                                                                                                     /gene= "megBII-1(megDVII)"
/product= "TDP-4-keto-6-deoxyhexose
/note= "encodes AAB82209"
                                                                                                                                                                                                                                                                                                                                  /gene= "megDV"
/product= "TDP-4-keto-6-deoxyhexose 4-ketoreductase"
/note= "eryVIV, dnmV homolgoue; encodes AAB82208"
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/gene= "megDIV"
/product= "TDP-4-keto-6-deoxyhexose 3,5-epimerase"
/product= "TDP-4-keto-6-deoxyhexose 3,5-epimerase"
/product= "eryBVIII, dnmU homologue, encodes AAB82207"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene= "megDIII"
/product= "daunosaminyl-N,N-dimethyltransferase"
/note= "eryCVI homologue; encodes AAB82206"
5592. .7197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene= ""megBVI(megT)"T"
deoxyglucose-"
note= "encodes AAB82201"
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                                                                                                                                                                                                                                                                                                                      complement (8228. .9220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /genë= "megY"
/producte= "mycarose O-acyltransferase"
/note= "encodes AAB82204"
(651. .5775
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/product= "TDP-megosamine glycosyltransferase'
/note= "eryCIII homologue; encodes AAB802203"
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product= "TOID-3-keto-6-deoxyhexose 3-aminotransaminase"
product= "eryCI, DnrJ homologue, encodes AAB82205"
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26230. .26733
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CC comprising a desonance biosynthetic gene cluster, a fragment or its CC biologically active variant, where the nucleic acid sequence is not CC derived from the eryC gene cluster of Saccharopolyspora erythraea or CC Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide CC biosynthetic gene cluster encodes proteins which synthesise methymycin, parbomycin or a combination of these CC empounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins CC are useful for synthesis of methymycin, pikromycin, neomethymycin and CC marbomycin. The alternative termination of polyketide synthesis may be cuseful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) CC monomers. The compounds produced by the recombinant host cells are useful cost as biopolymers, e.g., in packaging or biomedical applications, to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGGATCGGGGTGCGGGTCAGCGCAGGAAGCCGCGGGCCTCCTCCCAGCCGTCC
CCGGTGGTCTGCTCGTACTCCTCGTCGTTGAGGCCGTAGAGCGAGGTGCGGATGGCGTGC
                      CCGGTGGTGGCCTGGTACTCGTCGTTGTTCAGCCCGTACAGGGAGGTACGGACCGCCCG
                                                                                      GCGCGCAGCTGCTGGAAGCGGCGCAGGTTCTCGCGGACGCGGCGGAAGGCGGCCTTCTTG
                                                                                                               GCGCGCATCCGCAGGAAGTCCCCGGAGGTTCTTCCTGACCCGTTCGAAGGCGCCACGCTTG
                                                                                                                                                                         GAGGCACGGCCCGGGAGCACGATGTAGGCGAAGCCGAGGTTGATCGGCGACTCGCGCTCG
                                                                                                                                                                                                                TTGGCCCGCCCCGGCAGGATGATGTGGTTGAGGCCGAGCCGGACCGGTGCCGCCCGTTCG
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Pred. No. 3.9e-170;
0; Mismatches 876;
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AGGTCCCACAGGCCGGGCTGGCGGCGCAGGGTCTGTTCGGTGAGGGCGAAGGCGTTGGTG

SCAGCTCGCTGGTGTAGAGCGC 4288	229 GGGCGGGAGCGAGTGCACGGTGACGCCGCGTACGTCGCCGCAGCTCGCTGGTGTAGAGCGC	Oy 422 Db 1132
ACTGGTAGTIGCTCTCCTCGTC 4228	169 GATGCCGGTGGCGGTGCCGTCCACCAGGATGATCACGTACTGGTAGTTGCTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	Qy 416 Db 1126
CGCCTGCAGCCGGTCACGGTC 4168	109 GAAGTAGGGCTGTGCGACGACCTTCTCCGCGCGCAGGATCGCCTGCAGCCGGTCACGGTC	Qy 410 Db 1120
CATCTGGTGGCAGGCGGGGA 4108	)49 CTGTGTCAGCCGCAGCGGTGGCTCCGTGCGGTAGGGCGTCATCTGGTGGCAGGCGGGGGA	Qy 404 Db 1114
CCGTTCGGCGAGCCACTCGGT 4048	89 87	Оу 398 рь 1108
STCGCACACCCGGCGGATGTC 3988	29 27	39 110
FITCGCCTTGTCCCACTCCGC 3928	72	109
STCTTCATCGACGTGCGAACC 3868		109
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3GATGCGGCACCGGTGAGGCGG 3748	92	36 107
CGAGGCGCCGTAGTGGGCGGTG 3688	29 32	Qy 363 Db 1073
SCGAACCCGGCCCGTCCAGG 3628	69 72	Qy 350 Db 1067
GGGCCCTGCTCCACCGCCGTG 3568	09 12	Qy 350 Db 1063
AGCCTCCAACGCGCCGGCGGCG 3508	449 CCGACGCTGTACGGGAAGGCGGGCTCCCCGCCGTACCGCAGCCTCCAACGCCGCCGCGGCG 	Оу 34. Db 105
3CACGTCGGGCCGGGGTAGAGC 3448	92	Оу 33 Db 104
CACCGACTCCGCGTCGTACTTG 3388	2 9	Qy 33: Db 104:
CGTCGGGTTCTCCGACGGCACC 3328	269 TIGGTCAACGGTTCCAGGCCGCCGGAGAGGTACATCGCCGTCGGGTTCTCCCGACGGCACCC	Qy 3269 Db 10372
CACCAACGCCCCGATACCCGGG 3268	3209 TAGACGGTCAGGGCGAAGCCCCGCCGGGCGGCGTGCGACACCCAACGCCCCGATACCCGGG	Qy 32 рь 103

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GATCGCCAGATCGGTCGGTACGCGCTTCACG 5099	GTCGCCGATCGTCGGCCCACGTGCAGGGAGGCTGCAGGAACGCCTCGGGACCGCCGAA 5068	GCCGTTGGTGAGCCAGTTGTTGTTCAGGGCCCACTCCAGGCGGCCAGGAACCGCTGCCG 5008	GCAGTGCCGTACCCCGACCAGGTCGGCGACCCGGGCCTCGAACTCCCGCACCAGGGGCCC 4948	GGTGACGTCACCGGCCCCGCAGCACCAGTTCCAGGGCGACGGTGGCGTTGCAGGTGGCGAT 4888	GAGCCAGCTCGCCGCGTGCGCGGTGGCCGCGAAGGTCATTGACGGCATGATCACTTCACC 4828	GIGGTCCGGGTCGACCAGACCGGTCGCCGGGTCGACGAGAACACCCGGTGTGAGTCC 4768	TCGGCCCCACAGGTGTACGCCGACGATCGCGCCGGTCTGCGGGGTGACGAGCGCGGCGAC 4708	GAAGAAGAGCTTGACCTGGTGGTCGGCGGCGATCTTCGCCAGCGCCTCCACAGGTGCTGG 4648	GTCACCGGATCCGCCACCGGACGTCCACCCGTCGTGCAGCCCAGGGGGTGGGCGGCGTC 4588	CACCGCCCCCCCCCGAAGGCGGTGACCGCCTTGGTGGCGTGGAAGCTGAACACCTCGGC 4528	GCCGATGCCGAAGTTGTGCATGGCCCGGATCCGTTCGGCCAGCAGGCCGTCGTCGGTGAC 4468	GGCGGGGGGCACTCGCTCATCTTGCCGTTGGTGCCGATCTCGGTGACCACCTTGTCCGG 4408	GIGGTIGACCCGGTIGIGCCCCTGGICTÓGGCGAACGCGTCGAGGGAGGTGAGCCCCAT 4348

Streptomyces venezuelae desosamine gene cluster.

RESULT 6
AAD39043
ID AAD39043 standard; DNA; 13613 BP.
XX
AC AAD39043;
XX
DT 23-SEP-2002 (first entry)
XX
DT 8
Streptomyces venezuelae desosamine;
XX
KW Glycosylated polyketide; modified remaine; angucycline; angucycline; anthracycline; angucycline; anthracycline; polyether; an KW desosamine; des; gene; ds.
XX
OS Streptomyces venezuelae. Glycosylated polyketide; modified recombinant bacterial host cell; mRBHC; macrolide; anthracycline; angucycline; avermectin; milbemycin; tetracycline; polyene; polyether; ansamycin; isochromanequinone; sugar; desosamine; des; gene; ds.

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CDS
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(LIUH/)
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P-PSDB; AAE24228, AA
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                        AAE24234,
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                                                      Sherman DH,
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SHERMAN D H.
recombinant bacterial host cells in which the expression of nucleic acids encoding sugar biosynthetic enzymes has
                       AAE24235, AAE24236,
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encoded protein #1"
806. .2014
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                                                                                                                                                                                                                                  /product= "Streptomyces venezuelae
complement(11639. .10182)
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/transl_except= (pos:806. .808, aa:
/note= "CDS does not include start
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/transl_except= (pos:12881. .12883,
/note= "CDS does not include start
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/transl_except= (pos:8979. 8977, aa:Met)
/note= "CDS does not include start codon"
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/transl_except= (pos:7969. .7967, aa:Met
/note= "CDS does not include start codon
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/transl_except= (pos:4312, .4314, aa:Met)
/note= "CDS does not include start codon"
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'transl_except= (pos:3532. .3534, aa:Met)
'note= "CDS does not include start codon"
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3535. .4245
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complement(12883. .11636)
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Similarity 67.7%;
50; Conservative
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useful
Fig 8; 174pp;
                      for
                    producing metabolites
 English.
                      with altered
                    sugar
                      structures.
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The invention provides a method to alter the sugar structure diversity for a particular metabolite via the recruitment and collaborative action of sugar genes from a variety of sugar biosynthetic pathways to yield a metabolite comprising a non-natural sugar, e.g., a novel glycosylated polyketide. The invention also relates to a modified recombinant bacterial host cell (mRBHC) in which the expression and activity of nucleic acids encoding sugar biosynthetic enzymes has been altered. The mRBHCs may be cultured to produce the modified sugar products, e.g. a macrolide, anthracycline, angucycline, avermectin, milbemycin, tetracycline, polyether, ansamycin or isochromanequinone. The present sequence is Streptomyces venezuelae sugar (desosamine) biosynthetic gene cluster

BP; 1858 A; 4732 ü 5093 ູດ 1930 T; 0 U; 0 Other;

6

Length

13613,

GGGGGGATCGGGGCGGGTCAGCGCAGGAAGCCGCGGGCCTCCTCCCAGCCGTCC GGGCGGGTCGACGCCGTTCAGACGGCGCGGATCAGGCCCCGATGCTGATCCCCACCCGTCG Score 1309.4; DB 6 Pred. No. 3.9e-170; 0; Mismatches 876; 876; Indels 5, Gape 10218

GCGACGTCCCGTTCGAGTTGGGTTGAGCCGGGCGGTCACCGACTGGTCGAAACCGTCGAGG AGCCCGGGGAAAACCGGCCTCCCGGTACAGGTAGAACGTCTCCGAAGCAGGTCGATCTGCACC ACCTCGGTGAGGGAGGTGTCGGGGGTCACGCGGCCGCGATGTAGCGGGTCGCGCCGTCC acceaerecaecaecaecece a a construcción de la constr AAGTACTCGTCGCCGTCGACGGCCGCCACCTCGCCGCCGCCGCACGAAGTCCCTGACG AAGAACTCGTCCCCGGCTGCGGATCGATGCTGCGGCCCGACGTGACGAAGTCGTGGACG GCGGCGTCGCGCTCCAGCTGGTTCAGGCGGGCGGTGACGACCTGATCGAAGCCGTCCATG 2488 10456 2668 10398 2608 10338 2548 10278

TCGGCCCCGGTGCGCAGGCTGTTCAGGGCGTAGCCGTAGTCGATGTGGAGTCCGGGGGTG GCGACCTGCGGGTGCGCGGTGGCCATGGTGGCGGGCTTGATCCGCAGCAGTTCGGCG eccaccrecearreeecerceececarcerrerrrceecearcecarcecaacaecreeece 10578 2788 2728 10518

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Streptomyces venezuelae desosamine gene cluster coding sequence. narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence encodes a Streptomyces venezuelae desosamine gene cluster protein which was used the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid comprising a narbonolide polyketide syntha-
gene from Streptomyces narbonensis, useful for providing a
polyhydroxyalkanoate monomer for medical and industrial applications
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05-JUN-2000
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(first entry)
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/product= "PikB gene cluster protein
/product= "No initiation codon given in
/note= "No initiation codon given in
806. .2014
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complement(13706..15043)
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/product= "PikB gene cluster
complement(11271. .12149)
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6834. .7402
                                                                                                                                                                                                                                                                                                                                                /product= "PikB gene cluster protein #6 (AAY77208)"
/product= "No termination codon given in the specification"
/transl except= (pos:8270. .8272, aa:Thr)
/transl except= (pos:8273. .8275, aa:Thr)
/transl except= (pos:8276. .8278, aa:Gly)
/pomplement(10126. .11139)
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the specification"
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                                             (AAY77212) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated and purified nucleic acid segment cc comprising a desosamine biosynthetic gene cluster, a fragment or its comprising a desosamine biosynthetic gene cluster of Saccharopolyspora exythraca or compounds the eryC gene cluster of Saccharopolyspora exythraca or cc biosynthetic gene cluster crocodes proteins which synthesise methymycin, parknesses are useful for the proteins of biosynthetic gene cluster encodes proteins which synthesise methymycin, compounds. Recombinant or augmented cells comprising the desosamine cc and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins cc useful to prepare novel antibiotics and polyhetide synthesis are useful for synthesis of methymycin, pikromycin, neomethymycin and cc as biopolymers, e.g., in packaging or biomedical applications, to cc engineer PHA monomer synthases or to prepare biologically active agents, cc hromic obstructive pulmonary disease as well as other diseases involving respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine cc biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439, cc as given in figure 32. (Updated on 15-5EP-2003 to standardise OS field)
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Best Local Similarity
Matches 1849; Conserv
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P-PSDB; AAY77204, AAY77205, AAY77206, AAY77207, AAY77208, AAY77209,
AAY77210, AAY77211, AAY77212, AAY80998, AAY80999.
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AGGTCGGGGAAGCCGGCCTCGCGGTACAGGTACACGTCGCCGAGGAGATCGACCTGCACC
                                                                                                                                                                                                                                                                                                                   AAGAACTCGTCCCCGGCTGCGGATCGATGCTGCGGCCCGACGTGACGAAGTCGTGGACG
                                                          AGCCCGGGGAAAACCGGCCTCCCGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACC
                                                                                                                                                                                       ACCGAGTGCAGGCTCCGGTCCGGGGTGACCCGGCCGGCGACGTAGCGGGTGGCCCCCGCC
                                                                                                                                                                                                                                                        <u>AAGTACTCGTCGCCGTCGACGGCCGCCACCTCGCCGCCGCGCTCGACGAAGTCCCTGACG</u>
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                                                                              GTCGATGCGGTTGGGCCGCCCCACGAGGAGCGGCTGGTCGAAAGCGGCGGGGCCGCCGAA
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GAATGCGAGGTCGGATAAGGCGCTTTTCACG 12884
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RESULT 9
AAD 55810/c
ID AAD 55810 standard; DNA; 60196 BP.

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AAD 55810;
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PT 27-OCT-2003 (revised)
DT 07-AUG-2003 (first entry)
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Macrolide; rosaramicin; polyketide; polyketide synthase; PKS; enzyme;
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Micromonospora carbonacea.

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/partial 24993. .:
                          /product= "Polyketide synthase
46400. .47794
/*tag= j
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/product= "Polyketide
36292. .41016
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/product= "Polyketide synthase
5702. .19117
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/*tag= c
/product= "Polyketide synthase #10"
/note= "CDS does not include start
                                                                                 /product= "Polyketide
11049. .46403
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complement (1728. .2522)
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/note= "CDS does not include start
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/note= "CDS does not include start
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|9144. .24921
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1365. .5573
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The invention relates to genes and proteins involved in the biosynthesis of macrolides by microorganisms. In particular it relates to the nucleic acids forming the biosynthetic locus for rosaramicin (a 16-member macrolide antibiotic) from Micromonospora carbonacea. The invention is useful for the biosynthesis of macrolides by microorganisms. It allows direct manipulation of macrolides and related chemical structures by chemical engineering of the proteins involved in the biosynthesis of rosaramicin. It is useful to catalyse certain biochemical reactions, in vitro or in vivo, to direct or enhance the synthesis or modification of a vitro or in vivo, to direct or enhance the synthesis or modification of a vitro or in vivo, to direct or enhance the synthesis or modification of a vitro or in vivo, to direct or enhance the synthesis or modification of a vitro or in vivo, to direct or enhance the synthesis or modification of a vitro or in vivo, to direct or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the synthesis or modification of a vitro or enhance the vitro or enhance the vitro or enhance the vitro or enhance the vitro or enhance o
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AAE37001, AAE37002, AAE37003, AAE37004, AAE37005, AAE37006,
AAE37008, AAE37009, AAE37010, AAE37011, AAE37012, AAE37013.
                                           polyketide, polyketide substrate or its precursor. The present sequence is M. carbonacea polyketide synthase (PKS) type I gene cluster. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-2002
             Sequence
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/transl_except= (pos:51221. .51223, aa:Xaa)
/note= "Xaa corresponds to amino acids from position
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Pred. No. 6.7e-161;
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SULT 10	Db 57080 CCAGGAGCGACGCGTGGGGGGGGGGGTCGTCGTCGTGGTGGATCGCCCTCGGA 57021  Qy 4486 AGGCGGTGACCGCCTTGGTGGCGTGGAAGCTGAACACCTCGGCGTCACCGGATCGCCCA 4545
Qy       5500 GACCAGGAGGGC 5511                                 Db       56000 GTCCCGGATGAC 55989	4426 GCATGGCCCGGATCCGTTCGGCCAGCAGGCCGTCGTCGGTGACCACCGCCCCGCCCTCGA
Db 56060 CGGGGTGGCGGCGTCGGCTTGTTGATCACGACGAGGTCGGCACTCCCGCCGCGGCGTCCAC 56001	OY 4366 TCATCTTGCCGTTGCCGATCTCGGTGACCACCTTGTCCGGGCCGAATGCCGAAGTTGT 4425
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5320 GCGGATCTGGGTACGCGGACGTCCAGCACGTAGGTCGAGGTAGGT	OY 4246 CGGTGACGCCGCGTACGTCGCGCAGCTCGCTGGTGTAGAGCGCGTGGTTGACCCGGTTGT 4305
5280 CATGTACCGGTTCTCGGTTAGAACCGCCCACCCTCCTCGAAGTCCAAGGCCTCGTA	QY 4186 CGTCCACCAGGATGATCACGTACTGGTAGTTGCTCCTCGTCGGGGGGGAGCGAGTGCA 4245
\$200 GGTCATCCACGGTGGGGGGACCCCCCCCCCACGGACGACGACGACGACGACGA	Qy 4126 CGACCTTCTCCGCGCGCAGCATCGCCTGCAGCCGGTCGATGCCGGTGGCGGTGC 4185
5145 GCAGCTGATGTTGACGTAGTGGCTGTCGCGAGCAGTTCGGTGATCTTGGCCGAA	OY 4066 GTGGCTCCGTGCGGTAGGGCGTCATCTGGTGGCAGGCGGGGGAGAAGTAGGGCTTGCGGA 4125  Db 57440 GCTGCCGGGACCGGTAGGGCTCCAATTGGTGACAGGCCGGCGAGAAGTAGCGCTGCGCCA 57381
5086 56420	QY 4006 GGCCGGTCGGAGGGCGAGCACCCGTTCGGCGAGCCACTCGGTCTGTGTCAGCCGCAGCG 4065
5026 GGCCCACGTGCAGGGGTGCAGGAACGCCTCCGGACGCCCGAAGATCGCCAGATCGGTCG	OY 3946 TGGTGGTGGCGAGTCGCGCGCGACACCCCGGCGGATGTCCTCACTGGACACCCGAGG 4005
4966 TETTGTTCAGGGCCCACTCCAGGCGGCCAGGAACCGCTGCCGGTCGCCCGATCGTCGGCC	QY 3894 CACGAACCGTTGCGTTTCCGCTTGTCCCACTCCGCGTTGATCAACGCACCGC 3945  Db 57620 CCACGCTCTGTCCGGCCCGGGCTGCTGCCACCGAGCGGTCAATTCCGAATCCCC 57561
4906 56600	QY 3835 CGCCGTAG-GAGTGGTCTCATCGACGTGCGAACCCTTCTGGCGTCTGTGGTGCGAGAGAT 3893
4846 56660	OY 3775 CACGGCCGGCCGGCGTCGGGTCGGGTCCGCGATCTCCGTCGGTACGGCGGT 3834
4786 56720	OY 3715 TTCGGCGGTGTCGGATGCGGCACCGGTGAGGCGGGTGACCTCGGCGCTGAGCGCCCGCAC 3774
	QY 3655 CGGGGTGAACGGCGCGTAGTGGGCGGTGAGTTCGGCGAGCCGGACCGCCTGTCG 3714
(D	QY 3595 GTCGAGCAGCTCGCCGAACCCGGCCCGGTCCAAGGTCGAACCGGCGCGCATCTGCTCCAA 3654
QY 4606 GGTGGTCGGCGGCGATCTTCGCCAGCGCCTCCACAGGTGCTGGTCGGCCCCACAGGTGTA 4665	QY 3535 GTACTTGCCCGCCGGGCCCTCCACCGCCGTGCCCAGCTGCGGGATGCGAACAG 3594
Db 56960 CCGGGCCCTGTGAGGTGCACCCGATGGCGTGGGCGTCGAAGAACAAGAGCTTGACCT 4605  Db 56960 CCGGGCCCTGTGAGGTGCACCCGATGGCGTGGGCGTCGAAGAACAAGAGCGCAGGC 56901	OY 3475 CCGCCGTACCGCAGCCTCCAACGCGCCGGCGGCGGCGTTCAGCCGGCCTGATCGTGTTCCTCTCCACGCGTCCACGCGGCGCGCGC
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Best Local Similarity
Matches 1778; Conserv
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ADM45927,
ADM45934,
ADM45941,
ADM45948,
ADM45955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel polynucleotide, specifically a biosynthesis gene, comprising a nucleotide sequence which encodes a protein, where the gene is concerned with the biosynthesis of midecamycin. The polynucleotide of the invention demonstrates antimicrobial activity and may be useful for the biosynthesis of midecamycin, as well as for manufacturing macrolide compounds other midecamycin. The current sequence is that of the Streptomyces mycarofaciens midecamycin polyketide synthetase (PKS) DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrolide; midecamycin biosynthesis;
antimicrobial; ds; gene.
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                TCCCGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACCGCCACCTGCGGATGGGCG
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28-MAY-1998;
28-AUG-1998;
22-SEP-1998;
08-FEB-1999;
20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Narbonolide synthase; polyketide synthase gene; narbonolide polyketide; antibiotic; C12-hydroxyalse; picK; desosamine biosynthesis; desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme; picromycin biosynthesis; ss.
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Ashley Ó **Betlach** ď, Betlach 3 Tang ŗ Mcdaniel

New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value.

Disclosure; Col 45-48; 117pp; English

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The present sequence is used to produce the recombinant DNA compounds of the invention. The specification describes a recombinant DNA compound expressing recombinant polyketide synthase genes in host cells for the production of narbonolide, narbonolide derivatives and polyketides that are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis) of the compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant host ity of

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   TTGGTGAGCGGCTCCAGGCCGGCCGGAGAAGTACATCGCCGAGGGGTTGCCCCGCGGGTATC
                       TTGGTCAACGGTTCCAGGCCGCCGAGAGGTACATCGCCGTCGGGTTCTCCGACGGCACC
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Pred. No. 7.5e-91;
0; Mismatches 476;
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22-SEP-1998;
08-FEB-1999;
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                       Betlach
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Narbonolide polyketide synthase; ketolide; PICCV; picromycin; anti
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                                                      Streptomyces
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                                                                                                                                                                                                                                                           standard; DNA;
                                                                                                                                                                                                                                                                                                                                                    CGTTCGGCCGGGGCGGTGGCGGAGAGGGCGGCGGGCGGTCATCGGGAGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTCGGCGAGCCGGACCGCCTGTCGTTCGGCGGTGTCGGATGCGGCACCGGTGAGGCGG
                                                                                                                                               from cosmid pKOS023-27 from Streptomyces venezuelae.
                                                        venezuelae
                                                                                                                                                                                   (first
49. .1507
                  Location/Qualifiers
                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                             1565
                                                                                        ase; PKS; cosmid pKOS023-27; antibiotic production; narbo
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                                                                                              narbomycin;
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27-MAY-1999;
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98US-0087080P.
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This is contig 005 from the recombinant cosmid pKOS023-27 DNA sequence CC (see AAZ56001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS. CC (Polyketides are compounds synthesised from 2-carbon units through a coding sequence modifications. Modular PKSs are CC responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules, and two thioester domains. Four proteins make up the narbonolide PKS (CPICAI, PICAII and PICAIV). PICAI includes extender modules and 2, PICAII includes extender module 6 (PICAI, PICAII includes extender module 5 and 4, occombinant form the PICB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant CC instead proteins can be isolated in recombinant form from the recombinant CC commid pKOS023-27. Narbonolide is desosaminylated in S. venezuelae to CC vield narbomycin, the desosamine biosynthetic genes are also found in CC expression, and the desosamine biosynthetic genes are also found in CC express, in transformed cells, narbonolide (or its derivatives) or other enzymes recombinantly expressed in the same hosts) to polyketide con this form the recombinant promoter of the protein intermediates. The antibiotics are useful in human cc or veterinary medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 68.1
Matches 1015; Conservative
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P-PSDB; AAY67210.
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TCGGACAACCTGCCGTCGTCCCGACCGCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGC 2908
                                                                                                                                                                                                                                                                                                                                                                                         AAGAACTCGTCCCCCGGCTGCGGATCGATGCTGCGGCCCGACGTGACGAAGTCGTGGACG 2548
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                                                                                                                                   COCTCGCCGCGTAGTCGACGAACCGGGCGAGGCCCTCCCGCAACTCGGTCCGTTCGCCC
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                                                                   CGCTCGCGGACCCGCTCCTCGAAGGCGTTGAGGGCCTCCTGGAGCTCGGCCCGCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTCGGGGAAGCCGGCCTCGCGGTACAGGTACACGTCGCCGAGGAGATCGACCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCCCGGGGAAACCGGCCTCCCGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACC
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	CGTTCGGCCGGGCGGTGGCGGAAAAGGGCGGGCGGTCATCGGGAAGCGTC 40	90	밁
	TCCGCGATCTCCGCTCGGTACGCGGTCGCCGTAGGAGTGGTCTTCATCGAC 3859	3809	Ş
91	GCGAGGGTCTGGCCGACGGCGTGGACCGCCCCCCAGATCGGCTCCGGGGTGCGCGCAG	150	뮹
3808	GTGACCTCGGCGCTGAGCGCCCGCACCACCGCCGGGCGGG	3749	S
151	AGCCGGACGAGGTGGCGGGCGGTCGTTCCGGCCTCGTCGGGCGCACGAGGCCGCCGCCG	210	닭
3748	AGTTCGGCGAGCCGGACCGCCTGTCGTTCGGCGCGCGTGTGCGGATGCGGCACCGGTGAGGCGG	3689	Ş
211	cccaggregregeegectectecagegggggaaaggggetgttgeeggagegeagege	270	밁
3688	TCGAACCGACGCGCATCTGCTCCAACGGGGTGAACGGCGAGGCGCCGTAGTGGGCGGTG	3629	S
271	CGGAGCTCCGGGACCTGCCCGAACAGGGCGAGGAGGCGCCGGAAGGCGTCCCCGGTCGACG	330	밁
3628	CCCAGCTGCGGGATGCGATCGAACAGGTCGAGCAGCTCGCCGAACCCGGCCCGGTCCAGG	3569	Ş
331	TCGAGCGGGAGCAGGGTGTTCTTCCAGTACGCCCCGGCGGGGCCGGTCTCGACCGCGGTG	390	망
3568	TTCAGCGGCCTGATCGTGTTGCTCCAGTACTTGCCCGGGCCCTGCTCCACCGCCGTG	3509	Ş
391	CGACGCTGTACGGGAAGACGGGCTTCCTGGCGAGGCGCCGCGTCGAAGACGCCGCCTGT	450	밁
3508	CCGACGCTGTACGGGAAGGCGGGGCTCCCGCCGTACCGCAGCCTCCAACGCGCCGGCGGCG	3449	Ş
451	GCGCCGGTCACACGGACGCAGAAGTGGCAGCGGAACATGCAGGTCGGGCCGGGGTAGAGG	510	문
3448	GCACCTGTCACCCGTACGCAGAAGTGACAGCGGAACATGCACGTCGGGCCGGGTAGAGC	3389	S
511	TCGTCGATGACCGACCGGAACATGGCGTTGCCGGCGTCGAGGGGCGGACGGGTCGTAGCGG	570	문
3388	TCGTCGATGACCGAGGTGAGGATCTCGTTGCCGGGCCACCGACTCCGCGTCGTACTTG	3329	S
571	TTGGTGAGCGGCTCCAGGCCGCCGAGAAAGTACATCGCCGAGGGGTTTGCCCGCGGGTATC	630	닭
3328	TIGGTCAACGGTTCCAGGCCGCCGGAGAGGTACATCGCCGTCGGGTTCTCCCGACGGCACC	3269	\$
631	TAGACGGTGGGCCGCAGGCCGTGGTCGGCGTGCGCGGCCAGGCTCCCGAGGCCGGGG	690	뫄
3268	TAGACGGTCAGGGCGAAGCCCCGCCGGGCGGCGTGCGACACCAACGCCCCGATACCCGGG	3209	ঠ
691	AGGCCCCAGAGGCCGGGCTGGCGCTCCAGGGTGCGCTCGGTGAGCGCGCGAAGGAGTTCGTG	750	뫄
3208	AGGTCCCACAGGCCGGGCGCGCGCGCGCGCTCTGTTCGGTGAGGGCGAAGGCCGTTGGTG	3149	Ş
751	CCGGTGGTCTGCTCGTACTCCTCGTTGAGGCCGTAGAGCGAGGTGCGGATGGCGTGC	810	Ъ
3148	CCGGTGGTGGCCTGGTACTCGTTGTTCAGCCCGTACAGGGAGGTACGGACCGCCCG	3089	ð
811	GCGCGCAGCTGCTGGAAGCGGCGCAGGTTCTCGCGGACGCGGCGGAAGGCCGCCTTCTTG	870	닭
3088	GCGCGCATCCGCAGGAAGTCCCCGGAGGTTCTTCCTGAACCCGTTCGAAGGCGCCACGCTTG	3029	Ş
871	GAGGCACGGCCCGGGAGCACGATGTAGGCGAAGCCGAGGTTGATCGGCGACTCGCGCTCG	930	뮍
3028	TTGGCCCCCCCGGCAGGATGATGTGGTTGAGGCCGAGCCGGACCGGTGCCGCCCGTTCG	2969	ð
931	GTCCTGCCCTGCCCGGCGTCGTTGAGGTCGGCGATGAAGTCGACCAGGTCGAGCAGGCAG	990	망
2968	geccegrecagecregacregarreagregaceagregargaacreagregargageceg	2909	Ş
991	TGCGGCAGCTTGCCGTCACGGCCGCTGTAGTCCTCGCGAATGTTGACGAAGTCGATC	1050	벙

RESULT 13 ADA09423/c ID ADA094 XX AC ADA094 ADA09423; ADA09423 standard; DNA; 1565 BP

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Best Local Similarity
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06-MAY-1998;
28-MAY-1998;
28-AUG-1998;
22-SRP-1998;
08-FEB-1999;
20-MAY-1999;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces venezuelae; Sv; narbonolide polyketide synthase; PKS; narbonolide PKS; narbomycin biosynthesis; bicromycin biosynthesis; ptromycin biosynthesis; PKS gene cluster; picromycin; glycosylation; hydroxylation; C12 hydroxylase; PicK; desosamine biosynthesis; desosaminyl transferase enzyme; antibiotic; narbonolide synthase;
                                                                                                                                                                                                                                                                                                                                                                             Streptomyces venezuelae (SV) narbonolide polyketide Synthases (PKSS). The recombinant PKSs are derived from narbonolide PKS and other genes involved in narbomycin and picromycin biosynthesis in recombinant host cells. The invention also discloses the S. venezuelae PKS gene cluster that results in the production of picromycin. Also disclosed are enzymes such as those responsible for glycosylation and hydroxylation, (e.g. Cl2 hydroxylase (PicKI), desosamine biosynthesis, and desosaminyl transferase enzymes. The recombinant narbonolide, narbonolide derivatives, and polyketides are useful as antibiotics and as intermediates in the synthesis of compounds for pharmaceutical applications. The present sequence encodes S. venezuelae PICCV.
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22-SEP-1998;
08-FEB-1999;
08-MAY-1999;
27-MAY-1999;
The present invention relates to novel recombinant DNA compound that encodes a domain of a narbonolide polyketide synthase (PKS), a desogamin biosynthetic gene, a desogaminyl transferase gene or a beta-glucosidase gene of Streptomyces venezuelae, or a pick hydrolase gene of S. venezuelae. The recombinant DNA compounds are useful in expressing
                                                                                                                           New recombinant DNA compounds encoding a narbonolide polyketide synthase, useful for expressing recombinant polyketide synthase genes in host cells for the production of narbonolide and polyketides useful as antibiotics.
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Similarity 68.1%;
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WPI; 2003-041412/03

of polyketides by recombinant DNA technology, useful as and as intermediates in the synthesis of pharmaceutical

The present invention relates to recombinant DNA sequences encoding for narbonolide polyketide synthase (PKS) domain, and methods of producing polyketides by recombinant DNA technology. The recombinant DNA sequences are derived from Streptomyces venezuelae desosamine biosynthetic, desosaminyl transferase, beta-glucosidase, or pick (C12) hydroxylase genes. The method is useful for transforming a cell with a recombinant expression vector that encodes a functional beta-glucosidase gene, and therefore for increasing the yield of a desosaminylated polyketide in a cell. The recombinant methods and materials are useful for expressing polyketides with significant antibiotic activity, derived in whole or in part from the narbonolide PKS gene, and other genes involved in part greent sequence represents contain bosynthesis in recombinant host cells. The present sequence represents contain of S. venezuelae number of the presents contain the presents co containing

195 T; 0 U; 0 Other;

GGGCGGGTCGACGCCGTTCAGACGGCGCGGATCAGGCCCCGATGCTGATCCCACCCGTCG Score 729.4; DB 10; Pred. No. 7.5e-91; 0; Mismatches 476; Indels Length 0, Gaps 2428 0

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c 3	3037.4	34.0	8160	σ	AX000487	AX000487 Sequence
C 4	3032.6	33.9	8051	σ	AR092722	AR092722 Sequence
ი 5	3032.6	33.9	8340	ш	SEU77459	U77459 Saccharopol
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c 18	913.8	10.2	1206	D	AX000494	AX000494

## ALIGNMENTS

	CDS	gene	source	FEATURES	COMMENT	JOURNAL	TITLE	AUTHORS	PUBMED	JOURNAL			TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE						KEYWORDS	ACCESSION	DEFINITION	Locus	SEERYGENE/c	
<pre>/gene="EryBIV" /function="involved in mycarose biosynthesis" /codon_start=1</pre>	/gene="BTYBLV" 2421210	/organism="Saccharopolyspora erythraea" /mol_type="genomic DNA" /strain="NRRL2338" /db_xref="taxon:1836" _421210	18160	Location/Qualifiers	University Of Cambridge, Tennis Court Road, Cambridge CB2 1QW, UK Related sequence: L05776.	P.F. Leadlay,	Direct Submission	Leadlay, P.F.	•	Mol. Gen. Genet. 256 (3), 239-251 (1997)	erythraea	erythromycin biosynthetic gene cluster in Saccharopolyspora	seven genes from the	Gaisser, S., Bohm, G.A., Cortes, J. and Leadlay, P.F.		.bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspora.	Bacteria: Potisobatoria: Potisobactorião, Potisomiotalos.	Saccharopolyspora erythraea	TDP-N-dimethyldesosamine-N-methyltransferase.	TDP-4-keto-6-deoxyqlucose 5 epimerase;	qlycosyltransferase; TDP-4-keto-6-deoxyglycose 3.5 epimerase;	eryCIV gene: eryCVI gene: erycVI gene; erythromycin:	reductage: ervBIV gene: ervBVI gene: ervBVII gene:	2.3 dehydratase: aminotransferase: dehydrase: deoxyhexose	¥11199	ea erythromycin gene cluster DNA.	SEERYGENE 8160 bp DNA linear BCT 18-APR-2005		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQYLEGGPSGRGLFVGVRG"
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LGDVRGISVHAFDPGBEQNNYQYVIISVDSAATGIDRDCLQAILRAEKVVAQPYFSPGC

HQMQFRTEPPLRLENTEQLSDRVLALPTGPAVSSEDIRRVCDIIRLAATSGELINAQ
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6080. .7549

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                                                                                                                                                                                                                                                                          34.0%;
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                                                                                                                                                                                                                                              Score 3037.4; DB 1;
Pred. No. 2.1e-207;
D; Mismatches 863;
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gene

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CCCGACGCTGTACGGGAAGG 3                      CCGACGCTGTAGGGGAAGG 6				<u>ი</u> —ი	CCGGGCT	CTGGTACT		CGCCCCGGCAGGA	HH	CGTCGT		ი—ი						
3467 6468	3407 6528	3347 6588	3287	3227 6708	3167 6768	3107	3047	2987 6948	2927 7008	2867	2807 7128	2747 7188	2687 7248	2627 7308	2567 7368	2507 7428	7488	7548
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4488 GUGTGACUGUTTIGING	507	567	308 627	687	188 747	128 807	4068 GUCTCCGTGCGGTAGGGCC	4006 CCGTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3948 GTGGTGGCAATGACGTCGCACACCCGGCGATGTCCTCACTGGACACCGACGGG	3888 GAGGATCACGAACCGTTGCGTTTCCGCTTGTCCCACTCGCGTTGATCAACGCACCGCTG	3828 GGGGGTGGCGFAGGAGFGGTCTTCATCGACGTGGAACCCTTCTGGGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG	3768 CCCGCACCACGGCCGGCCGGCTCGGCGTCGCGCATCTCCGTCGGTA	3708 CCTGTCGTTCGGCGGTGT           6227 CCTGCACGTCGGCGTCAC	6287 GCTCCAGCGGCGTGAACG	6347 CGAACAGGTCGAGCAGGT	6407 TGGACCAGTACTTGCCCG	6467 CAGGCTTGCGGTAGACCG	3468 CGGGCTCCCGCCGTACCG
GAGGTGACCGCCTTCGTGGCGTGGAAGCTGAACACCTCGGCGTACCGGATCCGCCCACC	A TOGET CONTENT OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE	ATCTTGCCGTTGGTGCCGATCTCGGTGACCACCTTGTCCGGGCGATGCCGAAGTTGTGC	308 TCCTRGGTCTCGGCGAACGCGTCGAGGGAGGTGAGCCCCATGGCCGCGCGCG	GTGACGCCGCGTACGTCGCGGAGCTCGGTGGTGTAGACCCCGGTTGTGCGCGTTGTGCGCGAGTAGGCGCGTGGTTGAGCCCGGTGGTTGTGCGAGTAGGCGCGTGGTTGAGGCGGTTGTGC	TCCACCAGGATCATCACGTACTGGTAGTTGCTCTCCTCGTCGGCCGGAGCCAGTGCACG	ACCTTCTCCGCGCGAGGATCGCCTGCAGCCGGTCGATCCCGGTCGATGCCGGTCGCGCGCGCGCGGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGCGGGTCGCGCGGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGCGGTCGCGCGGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGTCGCGTCGCGTCGCGCGGTCGCGCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGCGGTCGCGTCGCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGGTCGCGGTCGGTCGCGGTCGGTCGCGGTCGGTCGCGGTCGGTCGCGGTTCGGTGGGTCGGTGGGTCGGTGGGG	068 GECTICGIGGGAGAGGGGGGGGAGAAGTAGGGTGGGGACA 127 	ACCCGITCGGCGAGCCACTCGGT                 ACCCGGTCGGAGAGCTGTTCGGT	ACGTCGCACACCCGGCGGATGTC	CGTTTCCGCTTGTCCCACTCCGC		GGTCGGCGTCGGGTCGTGCCGCG	CCTGTCGTTCGGCGGTCTCGGATGCGGCACCGGTGAGGCGGGGGTGACCTCGGCGCTGAGGG		CONACTOR OF CONTROL OT CONTROL OF	TOTAL CHARLES A CONTROL OF THE TABLE TO THE CONTROL OF TH	CAGGCTTGCGGTAGACCGCCGCGCGTCCAGTGCGCGCGTCCAGCGGCTTGATCGTGT	CAGCCTCCAACGCGCCGGCGGCG
GTCACCGGATCCG	ACCECCEC	GCCGATGCC		GIGGITGA          GIGGITGA	GGGCGGGA	GATGCCGG	GAAGTAGG	CIGIGICA       GITCTCCA	CTCACTGG	GTTGATCA          GTTGATCA	TCCTGGCA	TCGGCGAT	GAGACCTO	AGGTCGGC	CCGAGCCC	CCCAGGI	TCCAGCG	TTCAGCG

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5628 TGCCGTCGTCGCGGATCCACCCGCTGCGGTCGATGTCGGCCAACGGCCGGGTGCGTT 5687	5568 GGTGACTGGTCGTCACGGAGACGCCGAAGATGCTGAAGTACTTCTTGTCCTCGTGTTTCGA 5627	4427 GGGCAGCAGCCGTTGTTGGCGGGCAAGAGCAGCGGCTGCATCCACGAGTTGACCTCGC 4368	508 GGGCGAGCATGCCGTGGTTGGCTGGGGGGGGGAGAGCAGCGGGTTGCATCCAGGACCTCACCTCGC	5448 CCGCCTCGGTGCGCAGGTGCACGAGGCGCGTGGAAGGGTGCCGTCGATCTCCTTGACCAGGA 5507	5388 CGGTGTAGTTGTCCGGCTGACAGTGCACCGTCGCCGCCAACTCCGGCGACGTCGTGGCCAC 5447	5328 GGGTACGCGGGACGTCCAGCACGTAGTCGAGGTAGGTCGGGGGGGG	5268 GETTCTCGTTGCGGTAGAACCGCCCACCCTCCTCGGAGTGCCAGGCGTCGTAGCGGATCT 5327	5208 ACCGGTGGTCGGGGGCACCCCCCGTCGTCGAAGTCCGCGGGGCACCTCGACGAGCATGTACC 5267	5148 GCTGGATGTTGACGTAGTGGCTGTGCGCGAGCAGTTCGGTGATCTGGCCGAAGGTCATCC 5207	5088 ACGCGCTTCACGCCCGGCCGGCTGTAGACGGCGGACGGCGCAGGCGACGAGGCTGCGCA 5147	5028 CCCACGTGCAGGGGGTGCAGGAACGCCTCGGGACCGCCGAAGATCGCCAGATCGGTCGG	4968 TTGTTCAGGGCCCACTCCAGGCGGGCCAGGAACCGCTGCCGGTCGCCGATCGTCGGCCGA 5027	4908 AGGTCGGCGACCCGGGACCTCGAACTCCCGCACCAGGGGCCCGCCGTTGGTGAGCCAGTTG 4967	4848 AGCACCAGTTCCAGGGCGACGGTGGCGTTGCAGGTGGCGATGCAGTGCCGTACCCCGACC 4907	4788 GCGGTGGCCGCAAGGTCATTGACCGCATGATCACTTCACCGGTGACGTCACCGGCCCCC 4847	4728 COGGTCGCCGGGTCGACGTCGCAGAACACCGGTGTGAGTCCGAGCCAGCTCGCCGCGTGC 4787	4668 CCGACGATCGCGCCGGTCTGCGGGGTGACCGAGCGAGCGA	4608 TGGTCGGCGGCGATCTTCGCCAGCGCCTCCACAGGTGCTGGTCGGCCCCACAGGTGTACG 4667	4548 GGACGTCCACCCGTCGTGCAGCCCAGGGCGTGGGCGGCGTCGAAGAAGAGCTTGACCTGG 4607
RESULT	₽ :	& E	웅 &	₽ 5	5 음 :	& B :	& B :	\$ B &	S R 7	\$ B :	S B 8	S B &	S B &	? B 4	;	} B :	S B S	, B &	ם ס
2		GCCGCGACGGGAGAAGGTCC 6667	6588 CGTGCGGTACCGCCCGGACTGACATTACGACCC-CGCCCAGTGTAGGGCTCC 6646								TGTTGCCAGGTTAGTTGGCCTTGGCCTGCAGAGCGTGCAGTACGCCGTCGAACTCCGCACACACGTGCAGGTTCGGCCTTGGACGGCCTGCAGCGTGCAGTACGCCGTCGAACTCCCGCA		TGTICCGGTTGCCGCTCGCCCCCCCCCCCCCCCCCCCCC	TOTTTOCCOTTTTTCCCCACGAACTTCGGGACGCCCCGGACGTCGACGACGACGACGACGACGACGACGACGACGACGACGAC	CAACGARCCGCASCICCAISIICACCACGAIGIIGIIGIIGIIGIIGIIGIIGIIGIIGIIGIIGIIG		5/46 GENCLOGICUSCUCICUCICUCICUCICUCICUCICUCICUCICUCI		

Query Match Best Local Similarity 80.3%; Pred. No. 2.1e-207; Matches 3532; Conservative 0; Mismatches 863; Indels 6; Gaps 2;  Qy 2268 GANANANANANANANANANANANANANANANANANANAN	FT CDS 12102454 FT CDS 25103220 FT CDS 33084837 FT CDS 60807546 FT CDS 75788156 FT mat_peptide 242. FLocation/Qualifiers 18160 /organism="Saccharopolyspora erythraea" /mol_type="genomic DNA" /db_xref="taxon:1836"	/function = 'involved = 'eryCVI' /function = 'involved = 'eryBVI' /function = 'involved = 'eryBVI' - 'eryBVII' /function = 'involved = 'eryBVII' /function = 'pos /function = 'involved = 'eryBVII' /function = 'involved = 'cook!	Y/09458,12-UUN-11-UUN-IU-UUN-IUUN-I	ccharopolysporaerythraea and Streptomycesantibioticus tent: JP 2001511349-A 3 14-AUG-2001; ECHST MARION ROUSSEL Saccharopolyspora erythraea 14-AUG-2001 14-AUG-2001 21-JUL-1998 JP 2000504257	BD073332/c  Gene for biosynthesis and transfer of 6-deoxyhexose in Saccharopolysporaerythraea and Streptomycesantibioticus.  BD073332  VERSION SD073332  VERSION BD073332.1 GI:22618935  KEYWORDS JP 20015111349-A/3.  Saccharopolyspora erythraea  ORGANISM Saccharopolyspora erythraea  Bacteria; Actinobacteria; Actinobact
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	OY 4548 GGACGTCCACCCGTCGTGCAGCCCAGGGCGTGGGGCGTCGAAGAAGAAGACTTGACCTGG 4607
4367	Db 5447 GAGGTGACCGCCTTCGTGGAGGCTGGAAGACACCTCGGCGTTGCCGAAGGCGCCGACC 5388
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5508 GGCGAGCARGCCGTGGTTGGCGGGGGAGAGCGGTTGCATCCAGACCTCACCTCGC 556/	4428
	OY 4368 ATCTIGCCGTTGGTGCCGATCTCGGTGACCACCTTGTCCGGGCCGATGCCGAAGTTGTGC 4427
	Qy         4308 TCCCTGGTCTCGGCGAACGCGTCGAGGGAGGGAGGTGAGCCCCATGGCCGCGCGCACTCGCTC 4367         D           Db         5627 ACCCTGGTCTCGGCGAAGGGTCGAGGGAGGTGAGGCCCATCGCCGCGGCGCACTCGCTC 5568         D
4607 GCGAGCGCGGCACGTTCAACACGTAGTCCACATAGGCCGGCGAACTCCGCGGCGCGCGC	Cy 4248 GTGACGCCGCTACGTCGCCAGCTCGCTGGTGTAGAGCGCGTGGTTGACCCGGTTGTGC 4307
4667 GGTTCCGCGGGACGTCCAGCACGTAGTCGAGGTCGGGCGGTGTTCCTCGGGCACGT	Qy         4188 TCCACCAGGATGATCACGTACTGGTAGTTGCTCTCCTCGTCGGGCGGAGTGCACG 4247         D           LIIII
4727 ACCGGTGGTCGGGAGACCGCCACCCTCCTCGAGGCGGCTCGTAGCGGATCT	Oy         4128 ACCTICTCCGCGCGCAGGATCGCCTGCAGGCCGGTCACGGTCGATGCCGGTGGCGGTGCCG 4187         D
4787 5208	Qy 4068 GGCTCCGTGCGGTAGGGCGTATCTGGTGGCAGGCGGGGAGAAAGTAGGGCTGTGCGACG 4127
4847 GCGCGTTTCATCCGGCGGTCCTGGTGTAGACGGCCGAGGCGCATGCGCGATGATGCTGCGCA 4788 5148 GCTGGATGTTGACGTAGTGGCTGTGCGCGAGCAGTTCGGTGATCTGGCCGAAGGTCATCC 5207	Qy     4008     CCGGTCGGGAGCACCCCGTTCGGCGAGCCACTCGGTCTGTGTCAGCCGCAGCGGT     4067
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478 CUGGICGCUGGGICGACGICGCGGICGCGCGCGCGCGCGCGCGCGCGCG	Qy       3648       GCTCCAACGGGTGAACGGCGAGGCGCGTAGTGGGGGGGGG
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Mendez,C. and Salas,J.A.
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CARMEN (ES); SALAS JOSE A (ES)
Location/Qualifiers
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4668 CCGACGATCGCCCGGTCTGCGGGGTGACGAGCGCGGCGACGTGGTCCGGGTCGACCAGA 4727	3588 CGAACAGGTCGAGCAGCTCGCCGAACCCGGCCCGGTCCAGGTCGAACCGAACGGCGCATCT
4608 TGGTCGGCGGCGATCTTCGCCAGCGCCTCCACAGGTGCTGGTCGGCCCCACAGGTGTACG 4667	3528 TGCTCCAGTACTTTGCCCGCCGGGCCCTGCTCCACCGCCGTGCCCAGGTGCGGGATGCGAT
4548 GARCHICACCGICGIGCHGCCCAGGCGIGGCGGCGICGAAGAAGAGITTGACCTGG 5328 5387 GGCCGCCCGGCCGGCGGTGCAGCCCAGCGCGTCGAAGAAGAGITTGACCTGG 5328	Qy         3468         COGGCTCCCCGCCGTACCGCAGCCTCCAACGCGCCGGCGGCGGCGTTCAGCGGCCTGATCGTGT         3527           Q
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4428 AIGGECEGARICES EGGECAGECEGECES EGGECAGECECECECECECECEGARE 400	QY 3348 GGATCTCGTTGCCGGGGACCCACCGGGTCGTACTTGGCACCTGTCACCCGTACGC 3407
4368 ATCTTGCCGTTGGTGCGATCTCGGTGACCACCTTGTCCGGGCGATGCCGAAGTTGTGC 4427	3288 CGCCGAGAGAGGTACATCGCCGTCGGGTTCTCCGACGGCACCTCGTCGATGACCGAGGTGA 3347
4308 TCCCTIGGTCTTCGGCGAACGCGTCGAGGCAGGAGGCCCATCGCCCGCGCGCACTCGCTC *3507	Qy         3228 CCCGCCGGGCGGCGGCGACACCAACGCCCCGATACCCGGGTTGGTCAACGGTTCCAGGC 3287         Qy         1
4248 GIGALUCCUGUTACUTUGUGAGUTUGUTUGUTAGAGUTUGUTUGUTUGUTAGAGUTUGUTAGAGUTUGUTAGAGUTUGUGAGUTUGUTAGAGUTUGUTAGAGUTUGUTAGAGUTUGUTU	Qy 3168 GGCGGCGCAGCGTCTGGTTCGGTGAAGGCGTTTGGTGTAGACGGTCAGGGCGAAGC 3227
TCCACCASSATISATICACSTACTSSTAGTISCTCTCTCTCTCTCTCTCCTCCACGAATCGAACGCGTGCAACG	QY 3108 CGTCGTTGTTCAGCCCGTACAGGAAGGTACGGACCGCGAGGTCCCACAGGCCGGGCT 3167
ACCITCICCACAGATACCCTACAACATCCCCTCCCCCCCCCC	QY 3048 CCCGGAGGTTCTTCCTGACCCGTTCGAAGGCGCCACGCTTGCCGGTGGTGGTGCTTGCT
SCITCUS CUESTA CONTROL CONTR	QY 2988 TGATGTGGTTGAGGCCGGAGCCGGACCGCTTCCGCTTCCGCAGCATCCGCAGGAAGT 3047
CCGGICGGAAGGACCGAGAACACCCGGICGGAGAAGCACCGGGAGAAGTAAGGACTGTGTGCGAGCGGCAGCGGCAGCGGCAGCGGCAGCGGAGAGAGA	QY 2928 CGTTGAGTTCGACGATGAAGTCGACCAGGTCGATGAGGCGGTTGGCCCGGCCAGGA 2987
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AR092722 8051 bp DNA linear PAT 08-SEP-2000 Sequence 2 from patent US 5998194. AR092722 AR092722.1 GI:10019474 Unknown. Unknown. Unclassified. Unclassified.	528 GASTICGANGACIGATICACCIGATACGCCTCTCCGTGATGTGGGGGGTC				

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AUTHORS
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Polyketide-associated sugar biosynthesis genes
Patent: US 5998194-A 2 07-DEC-1999;
Location/Qualifiers
1. 8051
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                              ACCTTCTCCGCGCGCAGGATCGCCTGCAGCCGGTCACGGTCGATGCCGGTGGCGGTGGCGAGACTGCTCTCCGCTCGCAGGATCGCCTGCAACTGGTCGCGTCGATGCCGGTGGCCGTCGAGCTGGCGAG
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GUSCANGCURACUST CT TCCGSSTSGANCGACCAGCGTTCCATGGCGCTGAACGGCACGC GGGCGAGCCTGCCCTCGGGCTGGAACGACCAGCGGTCCATGGCGCTGAACGGCACGC	D 49	5268 GGTTCTCGTTGCGGTAGAACCGCCCACCCTCCTCGGAGTGCCAGGCGTCGTAGCGGATCT 5327	음 성
CCCACCGAAGITCGTCCGCACGTGCAAGCCCTCGAATGGAAGAAGAGCGCCCGGACTCGT	) B &	5208 ACCGGTGGTCGGGGGCACCGCCGTCGTCGAAGTCCGCGGGGCACCTCGACGAGCATGTACC 5267	음 성
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GARTCCGGTGGGGCGGGTCCCGTCGAAGTAACTGATGAACTGGACGCGGATCCGTTGT	, p &	4968 TTGTTCAGGGCCCACTCCAGGCGGGCCAGGAAACCGCTGCCGGTCGCCGATCGTCGGCCGG 5027	문왕
B TGTTGCGGTTGCGTTTGCGCAGGAACCAGGACCCTGCTCGACGACTGGAGGACGTCGACGA	B &	4908 AGGTCGGCGACCCGGGACCTCGAACTCCCGCACCAGGGGCCCGCGGTTGGTGAGCCAGTTG 4967	유 성
CANGGIVANGCOACCIGCASTICGGGIGGTCGGGGGGGGTCGAAGACCTCGACGACCA	p &	4848 AGCACCAGTTCCAGGGCGACGGTGGCGTTGCAGGTGGCGATGCAGTGCCGTACCCCGACC 4907	음 성
### GCACGGGCAGGTCCATGTTCACCACGTTGTCGTAGCGAGCAGCTGGG #################################	}	4788 GCGGTGGCCGCGAAGGTCATTGACGGCATGATCACCGGTGACGTCACCGGCCCGC 4847	음 경
806 GAASTCCSTCCAGTACCAGCCCAGCCTTCCACCTTGSTCGSTATGCAGGCCA 	) B &	4728 CCGGTCGCCGGGTCGACGTCGCAGAACACCGGTGTGAGTCCGAGCCAGCTCGCCGCGTGC 4787	음 성
	? B &	4668 CCGACGATCGCGCCGGTCTGCGGGGGTGACCGAGCGACGTGGTCCGGGTCGACCAGA 4727	음 중
B GANCGARCTCACGTGTGGTACGTCCGAGATCCAGCTCACAGGCTGTTCATGTTGT	, B &	4608 TGGTCGGCGGCGATCTTCGCCAGCGCCTCCACAGGTGCTGGTCGGCCCCACAGGTGTACG 4667	음 성
	, B &	4548 GGACGTCCACCCGTCGTGCAGCCCAGGGCGTGGGCGTCGAAGAAGAGCTTGACCTGG 4607	음 성
	}	4488 GCGGTGACCGCCTTGGTGGCGTGGAAGCTGAACACCTCGGCGTCACCGGATCCGCCCACC 4547	유성
	, B &	4428 ATGGCCCGGATCCGTTCGGCCAGCCGCCCGTCGTCGGTCG	음 성
	P & &	4368 ATCTTGCCGTTGGTGCCGATCTCGGTGACCACCTTGTCCCGGGCCGATGCCGAAGTTGTGC 4427	음 성
	) B 8	4308 TCCCTGGTCTCGGCGAACGCGTCGAGGGAGGTGAGCCCCATGGCCGCGCGCG	용 성
44 GCGAGCGCGGCACGTTCAACACGTAGTCCACATAGGCCGGTCGGAACTCCTCGGGCGCGT	D D	5524 GATATGCCGCGCACGTCGCGGAGCTCGTCGGAGTAGAGCCGCGTGGTTGAGGCGGTTGTGC 5465	뭥

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing and mutagenesis of genes from the erythromycin biosynthetic gene cluster of Saccharopolyspora erythraea tinvolved in L-mycarose and D-desosamine production Microbiology 143 (Pt 10), 3251-3262 (1997)
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Saccharopolyspora erythraea
Saccharopolyspora erythraea
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspora.

[ (bases 1 to 8340)
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Hutchinson, C.R. and Katz, L.
Direct Submission
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                                                                                                                                                                                                                                                                                                          /gene=
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                                                                                                                                                                                                                                                           gene="eryBIV"
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Matches 3529;
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Pred. No. 4.6e-207;
0; Mismatches 866;
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nigra megalomicin
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AAVVLFLVTGQAVGGRALI PMLLLIHAWFPALBISFGINPVSWSIACRAFFYLCFPLF
LFWISGIR FBERLMAMAAVVFAAIMAVEVVADLLLPSS PFLI PGLEYSA I GOWFILYTEP
ATRSLEFILGII LARILITGRWINVGLLPAVLLPFVFFVASLFLPGVYA I SSSMMILF
LVLI I ASGATADLQQKRTFMRNRVMVWLGDVSFALYMVHFLVI VYGADLLGFSQTEDA
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PVVTDGNEHVFYVYVVRHPRRDEIIKRLRDGYDISLNISYPWPVHTMTGFAHLGVASG
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           6535 ATGACCGTTGACCCGATCCCCCATACGCCTCTCCCGTGATGTCGTGGGCGGTCCGTGCGG
                                                                                                                                                                                                                                                                           2608;
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                GGGAGGTCCGCCGTGCCGAGTCAGGAAACGTATTGCCGATTGTGTGGATTCCGGAGTCGC
                                                                                                                                                                                                                         CTCGAGCCGATGCTCGGCGCGCGGGGGCCAACCAGTCGTGGACGTCGTCGGTGGCGGT
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99.9%;
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Score 2606.8;
Pred. No. 3.7e.
0; Mismatches
                                .7e-177;
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RESULT 7
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AUTHORS
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Patent: WO 0127284-A 1 19-APR-2001;
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ID NO: 7= translated amino acid sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FARAAYEQAFQRAGLSCSYVGHDLFSPGLFVGVAAEPGR"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="unnamed protein product; megDIV,
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SEQ:
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1-ketoreductase

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TDP-4-keto-L-6-deoxy-hexose 2,3-reductase; SEQ ID NO: 10=
translated amino acid sequence"
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WVLSRFGILGAVIGPRTPEQLDSALRAAELTLGEBELRELEAIFPAPAVDGPVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(10483. .11424)
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/-note="unnamed protein product; megBIV, TDP-hexose
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TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SBQ ID NO: 12= translated amino acid sequence"
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translated amino acid sequence"
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12181 . . 22821
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Best Local s
Matches 2608
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Sg

gg

Sg

CDS

RLPGGVTSPBEFWELLABGRDAVGGLPTDRGWDLDSLFHPDPTRSGTAHQRAGGFLTG
ATSFDAFFGLSFREALAVEQRITILELSWEYLERAGIPFTSLRTSRTGVFVGLIFQ
EYGFRLABGGEVEGYLMTGTTTSVASGRVAYLIGLEGPAISVDTACSSSLVAVHAG
QSLRRGESTMALAGGVTVMPTTGMLVDFSRWNSLAPDGRSKAFSAADGFGMAEGAGM
LLLERLSDARRHGHPVLAVIRGTAVNSDGASNGLSAPNGRAQVRVIRQALAESGLTPH

2608;

Conservative

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Similarity

29.28;

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                               TCACAGTCTTCAATCCGGGAGCGTTCTATGGCAGTTGGCGATCGAAGGCGGCTGGGCCGG
                                                                                        GGTAGTAGGCGATGCAGGCGTTTCGTCTCGCGCCCGGACGCGTCGCACTAGGTGGAATCCG
                                                                                                                                                                                                                      GGCCTGCGGAAACAGCATCGATCTGCGTCAGCCGTTCATTGCCCCCGGCGGCACCCGCCTT
                                                                                                                                                                                                                                                                CGTCGACATCACCGTGCAAGCCGCGATGACACCGACACCACGCCATGCTGGTGCCGCACT
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                                                                                                                                GGAAATCCGTGCCACCGGTCGTCCGCAGTGACGATCGCGGACCCGGGTTTCGAGACAGCA
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Pred. No. 3.7e-177;
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5 5	8395 CTGTCCCGTTCCGGGCCGGTGATCAGACGACGTCGGTCACCCGTCGCCCGTGGTCTCTCAGC 8454	§ 5
REFI AL	1921 GCCCTGGTGGCCACCCTGGCCACGCGACGCCGCGCCGGCCG	망
51	8335 GCCCTGGTGGCCACCCTGGCCACGGCGGCGTGCGGCGCGCGC	Ş
REFI	1861 CGTGGCGGCGAAGATCCTGTCGTCCCGGCCCGGCACCGACCTCGAC 1920	용 5
	801 GTCGCCGCGGCGAACCGTGATCCCGAAGGTCTTCACCGATCCCGACCGGTTCGACGTGGAC	? 문
AC TJ	8215 GTCGCCGCGGCGAACCGTGATCCCGAGGTCTTCACCGATCCCGACCGGTTCGACGTGGAC 8274	ş
OF OF	8155 GCGTCGGACCGCCGGGTGGGCGGGGTCGACGTCCCGACCGGTGGCGAGGTGACAGTGGTC 8214	용 성
VERS KEYW SOUT	681 CGTGTGGTGACGGAGGTGTCGCGGACGAGTCCCACCTGGAACGCCGCACCGCC 174	당 5
ACCT	1621 GCCGTCACCGAAGCTTCCCCGAACTGCCGGCACCACCGACGACCGAC	₹ ₽
007	8035 GCCGTCACCGAGCTTCCCGAACTGGCGGCACGACGTTGCCGAACGACCCGGAGACCGCGACC 8094	Ś
AY62	7975 GCGGTGCTGGTGGGGGTGGCGGAGCTGGCGGCCAACACGGTGGGCAACCCCGTCCTG 8034	P &
Db	01 ACCGANCAGGCGCTGACCGCCCTCGACGAGATCGACGGGGTCACCGGCGGTCGGGACGCC 1	ᅡ
<b>S</b>	ACCGAACAGGCGCTGACCGCCCTCGACGAGATCGACGCGGTCACCGGCGGTCGGGACGCC 7	ঠ
Db	7855 TGGACCTCGGCGACCCGGGTATGCCTGGACGCCCAGGTCAGCCCGCAACAGCTCGCCGTG 7914	음 성
Q B		Db
Ş	7795 GTGCTGGCGCTCGGTACCGCGCCCCGCACTCAAGGGCGTGGACCCCGACCGTCTCCGGTCC 7854	ş
da	7735 CTGGTGACCGAGCTGGGGTCGCGCTTCGATCTCGTGAACCGACTTCGCCCGGGAGGTCCCG 7794	유 성
Q B		ъ Б
Ş.	ACCGAGGACGCGGCGTCGGTGACAGTGGACGCCGACTGGCTCCAGCAGCGGTGCGCCAGG 773	§ §
Db 4	7615 CAGGTGGCCCACTGCCCGGGGGGCCTCCTGGGCCGGCCCTTTCCGGGAGTTCTACGCCCGC 7674	\$ <b>\$</b>
מ עס	7555 GCCGAGGTGCTCGCCGATCCGGGCTTCACCCACGGCCCGACGCTGCCCGGTGGATG 7614	유 정
δ 8		Дb
g &	7495 GGACGGGGACCGTACGCCAGTCGGGCCGGAACGTGGGTGG	Ş
D <sub>D</sub>	7435 ATGCTCCTGTCCGGACGGAACGACCCCTGGACCTGGTACGAACGGTTGCGGGCCGCC 7494 1021 ATGCTCCTGTCCGGACGGACGACGACCCCTGGACCTGGTACGAACGGTTGCGGGCCGCC 1080	용 성
Q	1 GAGTTGCAGATGGCCCGGGGTCTCTACTGGGGGTTCCGGTGCCAACCGCGATCTGTACTCG 1	2 5
B &	75 GAGITTGCAGATGGCCCGGGGTCTCTACTGGGGGTTCGGTGCCAACGGCGATCTGTACTCG 7	. <i>S</i>
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SULT 8 623658 CUS FINITION

AY623658
Aeromicrobium erythreum putative transcriptional repressor and putative dehydrogenase/reductase genes, complete cds; erythromycin biosynthesis gene cluster, complete sequence; putative oxidoreductase and Liph genes, complete cds; monoamine oxidase gene, partial cds; and unknown gene.

AY623658 AY623658.2 GI:59723038

CESSION PRSION YWORDS URCE ORGANISM Aeromicrobium erythreum

FERENCE AUTHORS TITLE Propionibacterineae, Nocardioi 1 (bases 1 to 61845) Brikun, I.A., Reeves, A.R., Cerr The erythromycin biosynthetic Aeromicrobium erythreum Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Propionibacterineae; Nocardioidaceae; Aeromicrobium. erythreum

Ind. Microbiol. Biotechnol.

31 (7),

335-344

(2004)

Cernota, W.H., Luu, M. stic gene cluster of

Aeromicrobium .B. and

Weber, J

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and

Weber, J

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Campbell

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REMARK

2 (bases 1 to 61845)
2 (bases 1 to 61845)
Brikun, I.A., Reeves, A.R. a
Direct Submission
Submitted (11-MAY-2004) Pe
Chicago, IL 60612, USA
3 (bases 1 to 61845)
Brikun, I.A., Reeves, A.R. a
Direct Submission
Submitted (14-FEB-2005) Fe
Chicago, IL 60612, USA
Sequence update by submitt Fermalogic, and

Fermalogic, Inc., Ξ. Campbell Park Drive,

Weber,J

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COMMENT
FEATURES
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CATGTTGCGGTTGCGTTTGCGCAGAACCAGGAACCTGCTCGGACTGGAGGACGTCGAC	ο φ Ο γ	4906 CCAGGTCGGCGACCCGGGCCTCGAACTCCCGCACCAGGGGCCCGCTGGTGAGCCAGT 4965
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686 TIGARCGARCTCACCIGIGGIGCGIACGICCAGANCCAGCAGCAGGIGGITCANGIT	) p &	4606 GGTGGTCGGCGGCGATCTTCGCCAGCGCCTCGACAGGTGCTGGTCGGCCCCACAGGTGTA 4665
	) B &	4546 CCGGACGTCCACCCGTCGAGGCCCAGGGCGTCGGAGGAGGAGAAGAAGAGCTTGACCT 4605
	, p. &	4486 AGGCGGTGACCGCCTTGGTGGCGTGGAAGCTGAACACCTCGGCGTCACCGGATCCGCCCA 4545
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CCACCOSTOSTICOSOGGACTOCTOCAAGTICOGGGGACCTCGACGAGCATGTA	) B &	4126 CGACCTTCTCCGCGCGCAGGATCGCCTGCAGCCGGTCAACGGTCGATGCCGGTGGCGGTGC 4185
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                                               Submitted (15-UUL-2002) Haruyasu Kinashi, Hiroshima University, bepartment of Molecular Biotechnology, Graduate School of Advanced Sciences of Matter; 1-3-1 Kagamiyama, Higashi-Hiroshima, Hiroshima 739-8530, Japan (E-mail:kinashiæhiroshima-u.ac.jp, Tel:81-824-24-7869, Fax:81-824-24-7869)
The nucleotide sequence has been determined by using restriction fragments and nested deletion fragments of the ordered cosmid library of pSLA2-L.
pSLA2-L is 210,614 bp long with G+C content of 72.8 % and carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces rochei
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                           and Kinashi,H.

The large linear plasmid pSLA2-L of Streptomyces rochei has an unusually condensed gene organization for secondary metabolism Mol. Microbiol. 48 (6), 1501-1510 (2003)
                                                                                                                                                                                                                        Mochizuki,S., Hiratsu,K. and Kinashi,H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                       Hiratsu, K., Mochizuki, S. and Kinashi, H. Cloning and analysis of the replication origin and the telomeres the large linear plasmid pSLA2-L in Streptomyces rochei Gen. Genet. 263 (6), 1015-1021 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of two polyketide synthase gene clusters on the linear plasmid pSLA2-L in Streptomyces rochei Gene 246 (1-2), 123-131 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinashi,H., Fujii,S., Hatani,A., Kurokawa,T. and Shinkawa,H. Physical mapping of the linear plasmid pSLA2-L and localization the eryAI and actI homologs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces rochei plasmid AB088224
                                                                                                                                                                                                                                                                                                                                                                       Mochizuki, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nimi, O. and Kinashi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biosci. Biotech. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces rochei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB088224.1 GI:30698345
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                                    143 ORFs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACGATCAGACCGAGGAACCCGATCTCGGGTTGGACGATGATGGGTTGGATCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGTGCACCTCGAGCCGATGCTCGGCGGCGGTGGGCCAACCAGTCGTGGACGTCGTC
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                                                                                                                                                                                                                                                            (bases 1 to 210614)
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prediction was based on the unique codon usage in Streptomyces
b et al., Gene 30:157-66 (1984)) using the FramePlot program of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugino, H.,
                                                                                                                                                                                                                                                                                                                                                                     Hiratsu, K.,
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pslA2-L
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http://www.nih.go.jp/~jun/cgi-bin/frameplot.pl. Where possible we chose an initiation codon (atg, gtg, ctg or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13 bp before the initiation codon). If this could not be identified we chose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Three-fourths of the pSLA2-L DNA are occupied by biosynthetic genes (three PKS gene clusters for lankacidin, lankamycin and an unknown type II polyketide, a carotenoid biosynthetic gene cluster, many regulatory genes and others). The range of each biosynthetic gene cluster has been deduced by comparison with similar gene clusters in most cases and may be revised in future.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishikawa and Hotta (FEMS Microbiol Lett 174: 251-253 (1999)) as
                                                                                                                                                                                                                                                                                                          /translation="markpraligiplgilivavlapapaahasadtyvgotwaapptaa paadstyvedotlkogtwisuradsuradtyvgotwaapptaa paadstyvedotlkogtwisuradsuradtavavlapatava dpetdrivregerpsatilegtrospatavavlagdotlislylportpesstyvaa yohnevaagdotwaapplipostatywisurelsgusvotraagdotutedsitdeeht tldaerweddllærlieggiagtgyvnagiggrrliedbsitdeeht tldaerweddllærlieggiagtgyvnagiggrrliedbpsepsaaespaayege salkreddulgopgaravtulgundlgopgiaapasdevlæegliagyrglierah englkiygatitpeagdtigyetperearvagotwabeltagyrglierah englkiygatitpeagdtigyetperearvagotwabeltagyrglierah englkiygatitpeagdtigyetperearvagotwabeltagyrglierah englkiygatitpeagdtigyetperearvagotwabeltagyrglierah pathapatagbotyldedavlæddar pdhlledaydgggamarafpldslr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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SGRLGKDWAVVBDUTRIFSLRRLYMTATPRLWGLDEDAGAPGELVASMEDDPDGLFG
ARCFTLTLSEAIDRGICAPYQVVCVDITDTQLQAAQLLGVBGRSDEVRGARLAALQTA
LLXASSBENFRRTLVFHHMVKEABAFAGLEDVAKRLHAAGDGLYPRTIWANNICGEH
LLXASSBENFRRTLVFHHMVKEABAFAGLEDVAKRLHAAGDGLYPRTIWANNICGEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPGHRRRVLGEFTSGIATDGTVVEKGFLGSVKVLGEGVDTRECDSVYWADVRGSMPDL
VQAVGRALRIQPGQGKVASLVVPVLLDPGETADNMLTSRPYNGLALLFRQAPLLTGHG
EEGFRAARFPGFEVRFVLGVNGAQRGASAGPASRSITPSAMSSLSISMRAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="N-terminal sequence is almost with that of ORF143 at the right end inner end of TIR-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to AE004736-10 protein (442 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   helicase, SCP1.136 inner end of TIR-L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to AL590463 Streptomyces coelicolor putative helicase, SCP1.136 (879 as); homology is seen untill
                                                                                                                                                                       similar to Y00459-2 Streptomyces protein, StrR (350 aa)"
                                                                                                                                                                                                                                                                                    complement (3659. .4645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trans1_table=11
/product="putative secreted
/protein_id="BAC76460.1"
/db_xref="G1:30698347"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (2315. .3595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Streptomyces
/mol_type="genomic DNA"
/strain="7434AN4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/protein id="BAC76461.1"
/db_xref="GI:30698348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1981/1992)
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/plasmid="pSLA2-L"
                                                                                                                                                                                                                                                   /note="ORF3 (328 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF2 (426 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="left terminal"
                                                                                                         codon_start=1/
transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (501 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 2188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat, TIR-L; shows
to TIR-R (complement
                                                                                                                                                                                                               griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeruginosa
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                                                                                                                                                                                                           regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4 %
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SdS

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/product="pyrroloquinoline quinone biosynthesis protein C"
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/db_xref="GI:30698352"
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AHRLGRLREHYPWIAEEGFEXFTARIEVVGPEGRSLLDLVARHAVSREQQEACVRALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (242 aa), lankacıdın protein (242 aa), lankacıdın (242 aa), l
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AGGPELVYVAADAYYDDRAFCPHOMGGSTQLTVTPAGDVLPCPAAYAITTLPVENALTRY
AGGPELVYVAADAYYDGRAFCPCTCPERHADHGGCRCQAFQLTGDAAATDPACGL
SPHRSLVDAALAEVTDGPVPAFVPRGPVPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4922. .5812)
/note="ORF4 (296 aa), lankacidin biosynthesis
similar to AE004625-4 Pseudomonas aeruginosa
pyrroloquinoline quinone biosynthesis protein
                                                                                                                                                                                                                                                                                                                                                                                                    /note="ORP8 (34 aa), lankacidin biosynthesis protein
similar to AL603642-197 Sinorhizobium meliloti putat
pyrroloquinoline quinone biosynthesis protein A (31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (6902. .7174)
/note="ORF6 (90 aa), lankacidin biosynthesis protein
similar to AL603642-200 Sinorhizobium meliloti putative
pyrroloquinoline quinone biosynthesis protein D (98 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5815. .6909)
/note="ORF5 (364 aa), lankacidin biosynthesis
similar to AJ277117-5 Gluconobacter oxydans pu
protein (359 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tränelation="MILLGTAAGGGFPQWNCACALCARGRRGELPARSQECVAVSGDG
RDWWLLNASPDIRTQLLAAPALTPGPGFRDTPVRGVLLTDAEVUHALGLAVLRGATGL
TVYAAPPVRGALSAELPVRGLLDRYAPWDWRDATAPGGFAVAGGLTVTAHPVGYTEAP
YAHAPDPDAPWVCATRIEDPATGGALVYAPCLATWPDGFDDLLASATCALLDGTFFSA
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                                            /product="pyrroloquinoline
/protein_id="BAC76466.1"
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces narbonensis partial sequence. AF521878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-JUN-2002) Biochemistry, University Road, Leicester LE1 7RH, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bate, N. and Cundliffe, E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   producer of narbomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bate, N. and Cundliffe, E.
The desosamine biosynthetic
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      2455 CCGGGCGGTCACCGACTGGTCGAAACCGTCGAGGAAGAACTCGTCCCCCGGCTGCGGATC
                                                                                                                                                                                                                               Similarity
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Sab gene

gene

CDS

gene

Conservative

14.7%;

Score 1313.8; Pred. No. 2.7e-0; Mismatches

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Indels

S.

Gaps

2514 10902 2454 ۲ Length 17665;

Sg

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11082 07 2694 111142 07 2754 07 2814 07 2814 07 2817 11362 07 2994 2994 2994 2994 2994 2994 2994 299	
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                                                                                                                                                                                                                                                                              Zhao, L., Liu, H.-w. and Sherman, D.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                             Xue,Y., Zhao,L., Liu,H.W. and Sherman,D.H.
A gene cluster for macrolide antibiotic biosynthesis in
Streptomyces venezuelae: architecture of metabolic diversity
Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12111-12116 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces venezuelae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence. AF079762
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VAVQVDLLGDVYLYEERGFPDLDGATTEYIAGRVTPDTSLTEVVRDFVERGGEVAAVDG
DEYFMDGFDQVVTARLNQLERDAADGWEEARGFLR"
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Gaymkntllpleqrgyfdaalarkpvppysvglypgptcmfrchfcvrvtgarydpsa
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/gene="desII"
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VARAYHRTYGLDVRITRCCNNYGPYQHPEKLIPLFVTNLLDGGTLPLYGDGANVREWV
HTDDHCRGIALVLAGGRAGEIYHIGGGLELTNRELTGILLDSLGADWSSVRKVADRKG
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Legferbefaaycetdhavgvnsgmdalqlalrglgigpgdevivpshtyiaswlavsa
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EGSLPraesfarqusdidthierpqalrvidavrewaervdqa"
ar i ralhnfgfdl pggs paggtnakms eaaaamgl tsldaf pev i drnrrnhaayreh
                                                                                                                                                                                                                      complement (10949.
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/protein_id="AAC68683.1"
/db_xref="GI:3789900"
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RANLAPVDADPRLRFVHGDIRDAGLLARELRGVDAIVHFAAESHVDRSIAGASVFTET
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/codon_start
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/transl_table=11
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/codon_start=
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/product="TDP-glucose-4,6-dehydratase"
/protein_id="AAC68681.1"
/db_xref="GI:3789898"
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/codon_start=
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/db_xref="GI:3789897"
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Sac

SdC gene

CDS gene

LADLPGVLVADHDRHGLINNHQYVIVEIDEATTGIHRDLVMEVLKAEGVHTRAYFSPGC HELEPYRGQPHAPLPHTERLAARVLSLPTGTAIGDDDIRRVADLLRLCATRGRELTAR HRDTAPAPLAAPQTSTPTIGRSR"

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Length

TTGGTCAACGGTTCCAGGCCGCCGGAGAGGGTACATCGCCGTCGGGTTCTCCGACGGCACC TAGACGGTCAGGGCGAAGCCCCGCCGGGCGGCGTGCGACACCCAACGCCCCGATACCCCGG GGCCGGTGCGGGCTGGACTCGTTGAGTTCGGCGATGAAGTCGACCAGGTCGATGAGGCGG CGCTCGGCGGCGTAGTCGACGAACCGGGCGAGGCCCTCCCGCAACTCGGTCCGGTTCGCCC TTGGTGAGCGGCTCCAGGCCGCGGAGAGAAGTACATCGCCGAGGGGTTGCCCCGCGGGTATC TAGACGGTGGGCCGCAGGCCGTGGTCGGTGGCGTGCGCCAGGCTCCCGAGGCCGGGG AGGCCCCAGAGGCCGGGCTGGCGCTCCAGGGTGCGCTCGGTGAGCGCAAGGAGTTCGTG CCGGTGGTCTGCTCGTACTCCTCGTCGTTGAGGCCGTAGAGCGAGGTGCGGATGGCGTGC CCGGTGGTGGCCTGGTACTCGTCGTTGTTCAGCCCCGTACAGGGAGGTACGGACCGCGCCG 3148 GCGCGCATCCGCAGGAAGTCCCGGAGGTTCTTCCTGACCCGTTCGAAGGCGCCACGCTTG GAGGCACGGCCCGGGAGCACGATGTAGGCGAAGCCGAGGTTGATCGGCGACTCGCGCTCG TTGGCCCGCCCCGGCAGGATGATGTGGTTGAGGCCGAGCCGGACCGGTGCCGCCCGTTCG AGTACTCGTCGCCGTCGACGGCCGCCACCTCGCCGCCGCGCTCGACGTCCCTGACG AGGTCCCACAGGCCGGGCTGGCGGCGCAGCGTCTGTTCGGTGAGGGCGAAGGCGTTGGTG GTCCTGCCCTGCCCGGCGTTGAGGTCGGCGATGAAGTCGACCAGGTCGAGCAGGCGG TGCGGCAGCTTGCCGTCGTCACGGCCGCTGTAGTCCTCGCGAATGTTGACGAAGTCGATC 10011 CGCTCGCGGACCCGCTCCTCGAAGGCGTTGAGGGCCTCCTGGAGCTCGGCCCGCTCCTCC TCGGCCCCGGTGCGCAGGCTGTTCAGGGCGTAGCCGTAGTCGATGTGGAGTCCGGGGGTG 9891 GCGACCTGCGGGTGCGCGTGGGCCGCATGGTGGCGGGCTTGATCCGCAGCAGTTCGGCG AGGTCGGGGAAGCCGGCCTCGCGGTACAGGTACACGTCGCCGAGGAGATCGACCTGCACC AGCCCGGGGAAAACCGGCCTCCCGGTACAGGTAGACGTCTCCGAGCAGGTCGATCTGCACC ACCTCGGTGAGGGAGGTGTCGGGGGTCACGCGGCCCGCGATGTAGCGGGTCGCGCCGTCC AAGAACTCGTCCCCCGGCTGCGGATCGATGCTGCCGCCCGACGTGACGAAGTCGTGGACG GCGGCGTCGCGCTCCAGCTGGTTCAGGCGGGCGGTGACGACCTGATCGAAGCCGTCCATG GCGACGTCCCGTTCGAGTTGGTTGAGCCGGGCGGTCACCGACTGGTCGAAACCGTCGAGG GGGGGATCGGGGCGGTGCGGGTCAGCGCAGCAAGCCGCGGGCCTCCTCCTAGCCGTCC GGGCGGGTCGACGCCGTTCAGACGCCGCGGATCAGGCCCCGATGCTGATCCCACCCGTCG ACCGAGTGCAGGCTCCCGGTCCGGGGTGACCCGGCCGGCGACGTAGCGGGTGGCCCCCCGCC 2608 Conservative 14.6%; 0; Score 1309.4; DB 1; Pred. No. 6.3e-85; 0; Mismatches 876; Indels <u>ν</u> Gaps 3208 3088 3028 2968 3268 10191 10071 9951 2848 10431 3328 10371 10311 10251 10131 9831 2728 9771 2668 9711 9651 2548 9591 2488 2428 9531

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Streptomycineae; Streptomycetales;
Streptomycetales;
Streptomycetales;
RS Sherman, D.H., Liu, H.W., Xue, Y. and Zhao, L.

DNA encoding methymycin and pikromycin
AL Patent: JP 2002536959-A 205-NOV-2002;
REGENTS OF THE UNIVERSITY OF MINNESOTA

OS Streptomyces venezuelae
PN JP 2002536959-A/2
PD 05-NOV-2002
PF 25-JUN-1999 JP 2000557373
PF 25-JUN-1999 US 09/J05537
PF 26-JUN-1998 US 09/J05537
PF 26-JUN-1998 US 09/J05537
PI DAVID H SHERMAN, HUNG WEN LIU, YONGQUAN XUE, LISHAN ZHAO PC
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12P7/ PC
42, C12P19/62,
PC C12N15/00, C12N5/00
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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DNA encoding methymycin and p
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Qy 4109 GAAGTAGGGCTGTGCGACGACCTTCTCCGCGCGCAGGATCGCCTGCAGCAGCCGGTCACGGTC 4168  Db 11207 GAAGTAGGCCGGTGTGCACGCCTTCAGGACCTCCATGAACGTCGCGGTG 1126  Qy 4169 GATGCCGGTGGCGGTGCACCACGAATGATCACGTACTGGTAGTTGCTCTCCTCGTC 4228	P P	3 11 3 6	Qy 3809 TCCGCGATCTCCGTCGGTACGCGTCCGTAGGAGTGGTCTTCATCGACGTGCGAACC	Db 10792 Adcocdancialerredecedecegrocarreceililler concentrate con	QY 3629 TOWARCHER CONTROLLER TO THE CONTROLLER T	3569 10672	Oy 3509 TTCAGCGGCCTGATCGTGTTGCTCCAGTACTTGCCGCGGGCCCTGCTCCACCGCGTG	QY 3449 CCGACGCTGTACGGGAAGGCGGCTCCCGCCGTACCGCAGCCTCCAACGCGCCGCGGCGCGCGC	Qy 3389 GCACCTGTCACCCGTACGCAGAAGTGACAGCGGAACATGCACGTCGGGCCGGGGTAGAGC	Qy 3329 TCGTCGATGACCGAGGTGAGGATCTCGTTGCCGGGGCACCACCGACTCCGCGTCGTACTTG	Db 10312 TAGACGGTGGGCCGCAGGCCGTGGTCGGTGGCGTGGCCGGGCCAGGCTCCCGAGGCCCGGGGCCGGGCCGGGCCGGGCCGGGCCCGGGGTTCCCGACGGCCCGGCAGGCCCGGGGTACATCGCCGGGGTTCCCGCGGGTATC

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                                                                                                                             Micromonospora griseorubida
Micromonospora griseorubida
Bacteria; Actinobacteria; Actinobacteridae; Actinomycet
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Micromonospora griseoru
macrolide mycinamicin,
AB089954
                                   Anzai,Y., Saito,N., Tanaka,M., Kinoshita,K., Koyama,Y. and Kato,F. Organization of the biosynthetic gene cluster for the polyketide macrolide mycinamicin in Micromonospora griseorubida PEMS Microbiol. Lett. 218 (1), 135-141 (2003)
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Pharmaceutical Sciences; 2-2-1 Miyama, Funabashi, Chiba, 27
Japan (B-mail:yanzai@phar.toho-u.ac.jp, Tel:81-47-472-2072,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anzai, Y., Saito, N
Direct Submission
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Qy 4501 TGGTGGCGTGAAGCTGAACACCTCGGCGTCACCGGATCCGCCACCCGGACGTCACCCGG Db 50538 TGGTGGCGTGAAGCTGAAGACCTCGGCGTCACCCGACCGGACGTCACCCCG Qy 4561 TCGTCGACCCAGGGCGTGAAGACCTCGACGTGCCCAAGACGCCCCTTGG Db 50598 CCGTGCACCCAGGGCGTGGACGAGAAGAAGAAGAACAGCTTGATCGTCGCGGCGACGATCGCCGAACAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	Db 50358 CGAAGGCGTCGGTCGGTCGGTGACCACCGCCCTCGAAGGAGGTTCACGACCT  Db 50368 CGAAGGCGTCCAGGGAGGTCAGTCCCATGGCGGAGGCCTCGCTCATCGTGGCGTTGG  Qy 4381 TGCCGATCTCGGTGACCACCTTGTCCGGATGCCGAAGTTGTGCATGGCCCGGATCC	50178 4201 50238 4261 50298	4021 50058 4081 50118		3607 GCCG 49638 GCGG 3667 CGAG 49698 TCGG 3727 GGAT 49758 TTCG 3787 GTCG 39818 GTCA

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Mechanism of the 2-deoxygenation step in the biosynthesis of the deoxyhexose moieties of the antibiotics granaticin and oleandomycin J. Am. Chem. Soc. 121, 2611-2612 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces antibioticus
Streptomyces antibioticus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                        A cluster of genes from Streptomyces antibioticus involved in the biosynthesis of the deoxysugar moieties of oleandomycin
                                                                                                                                                                                                                                         3 (bases 1 to 9523)
Park,S.-H.H., Sohng,J.-K.K., August,P.R. and Floss,H.G.
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                                                                                                                                                                                                                                                                                                                                       Park,S.-H.H.,
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TULSAKDTHAPSLAQAAETGILPDYEECRAYIAEAAGVGPAR"
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PVGPGLAAFVTRRIRGVLHVLLHARTEAGLLNGPEMAPTVQCRPLNYRAVPAEYRPAY
LDYVLSADPGRIRYDTLQSEEGGRFHHAENRYVVVEAEDDFPVEVPRDFRWLTLHQIL
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/note="Orf10; involved in the 2-deoxygenation dTDP-L-oleandrose biosynthesis"
/codon_start=1
/transl_table=11
/product="4-ketoreductase"
/protein_id="AAF59936.1"
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dTDP-L-oleandrose biosynthesis"
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/protein_id="AAP59933.1"
/db_xref="GI:7329193"
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/product="unknown"
/product="unknown"
/product="unknown"
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DRIABHLIALARRYGTEBPTPLESARRGLGLDRATFARVCHFCKPCVTGARYQQSA
LTDGNAMFASLLDRMPTUNPHALYLSGGLEPLTNPGTGDLVRRAAARGFKLSLYTNSF
ALTRQTLDRQPGLMDLYALRTSLYGLSEDDYVATTTKKGAFQRVKDNLTRFQALRRER
EAFVRLGLNYIILPGRAGRLTGLADYFADLNDAAPDRFVDETTRREDYSGRPDGKLAP
EERVELGLAVIIILPGRAGRLTGLADYFADLNDAAPDRFVDETTRREDYSGRPDGKLAP
EERVELGHGLAAFEERIRTRAPSLHVDYGYALQSLRIGVDAELPRIRFETMRPTAHPQ
VAVQVDLLGDVYLYREAGFPGLQCAERYVAGRLTTGTELSEVVRRFVTEGRQVAPRPG
EEYFLDGFDQTVTARLNQMETDIADGMAEHRGFLR"
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/codon_start=1
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AALAERF PGI VVNCAATTAVDDAETDEAAAALLNAEA PRLLAEAFAHGAFLYRLSTD
YVFPGDARTFYAEDHFTAFRSAYGRTKRDGEQAVLTALFTATVLRTAWLGRTGRSF
RTMIEREARGGAIDVVADQCGQPTWTGDLADRIIAVGHLPGVHGILHATWAGSATWYD
LAQEVFRLLDADFGRVRFTTGAAFRRFAFRFAYSVLGHDRWRGTGLAFLRDWRSALRE
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in dTDP-D-desosamine
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/protein_id="AAF59937.1"
/db_xref="GI:7329197"
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        GACCTGAAGTGCCACGCGCGTGCGCTCCTTGTCTTCCTTGTCTTCCGTTCGGATCGGGCC
                            GTCGGGTCGTGCGCGTCCGCGAATCTCCGTCGGTACGGCGGTCGCCGTAGGAGT-----
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                                                 Submitted (13-SEP-1999) Departamento Instituto Universitario de Oncologia Universidad de Oviedo, Oviedo 33006, Sequence update by submitter On Sep 16, 1999 this sequence version Location/Qualifiers
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Direct Submission
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Julian Claveria s/n, Oviedo, Asturias 33006, Spain
                                                                                                                                                                                                                                                                                                                                                   Identification and expression of genes involved in biosynthesis L-oleandrose and its intermediate L-olivose in the oleandomycin producer Streptomyces antibioticus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACGCCGTCGCCCGGTTGTAGACGGCGACGACGACGACGCTGCCAGCTGGATG
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                                                                                                                                                                                                   (bases 1 to 15052)
                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 9805)
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                                                                        version
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                     antibioticus
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de Asturias (I.U.O.P.F
Spain
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                                                                                                                                                                                      Mendez, C.
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                                                                        gi:3023163
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complement (1596. .3020)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="oleW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5037
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8225. .9682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="involved in L-oleandrose biosynthesis"
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4315 TCTCGGCGAACGCGTCGAGGGAGGTGAGCCCCATGGCCGCGGGGGCACTCGCTCATCTTGC 4374	Ş		
7759 CGGGGAGGCCGGAGAGTTCCTGCCGGTAGAGCTCGTAGTTGGCGCGGGTTGCTCGCGACCG 7700	Db <b>4</b> 3	3235 GGCGGCGTGCGACACCAACGCCCGGATACCCGGGTTCGTCAACGCTTCCAGGCCGCGGA 3294	유 성
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	Q B	3115 GTTCAGCCCGTACAGGAGGTACGGACCGCGCCGAGGGTCCCACAGGCCGGGCTGGCGGCG 3174	B 8
35 35	8 B 1	3055 GTTCTTCCTGACCCGTTCGAAGGCGCCACGCTTGCCGGTGGTGGCCTGGTACTCGTCGTT 3114	용 성
	S B &	2995 GITGAGGCCGAGCGGACCGGTGCCGCCGGTTCGGCGCATCCGCAGGAAGTCCCGGAGG 3054	р У
SCANGEGENERACTICGCACACCCGGCGGATGTCCTCACTGGACACCCGAGGGCCGGTCG	;	2935 TTCGGCGATGAAGTCGACCAGGTCGATGAGGCGGTTGGGCCCGGCCCGGCAGGATGATGTG 2994	ß 8
98 AACCETTGCGETTGCCC-TTGTCCCACTCCGGGTTGATCCACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	, B &	2875 GCTGTAGTCCTCGCGGACGGTGACGAAGTCGAGCGGCCGGTGCGGGGCTGGACTCGTTGAG 2934	유 왕
*/ - GATOTTCATCATCCATACCCTTCTGGCGTCTGTGGT	}	2815 GGCGAGGCCTCCCGCAACTCGGTCCGTTCGCCCTCGGACAACCTGCCGTCCTCCCGACC 2874	유 성
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bs GACCGCCCCACCACCACCGCCGGTCGGC   GC   GC   GC   GC   GC   GC	B &	2695 CATCGTTTCCGGCCGGATCCGCAACAGCTGGGCGTCGACACCCCGACGCAGGCTCTCCAA 2754	유 성
703 GACCGCCTGTTCGGCGGTGTCGGATGCGGCACCGGTGACCTCGGCGGT 359 GTCGGGTTCCAGTCCGGTGCCGGGGGGCGTCCTCCTCGATGAGGGGGGCAGTGCCGCGGC	}	2635 CAGGTAGACGTCTCCGAGCAGGTCGATCTGCACCGCCACCTGCGGATGGGCGGTCGGGCG 2694	g 8
*** CAGGGTGAAGGGTTTCGGTGCTGTAGCGTCAGGCTAGGTTTCGGCGAGCCGTAGCTGGTGAGCGGCTAAAGGTTCGGTGCTGTAGCGTTCGGCGAGCCGTAGCGTTAGCGTTCGGGGCTAAAGGTGCTCGGCGAAGCCGTAGCGTTAGCGTTCGGGGCTAAGGGTGCTTCGGGGAGCTAGCGTGTAGCGTTCGGGGCTAGCGGTGTAGGGTGCTTGGGGGGCTAGGGGTTAGGGTGTGTGGGGGGTAGGGGGTAGGGGGTAGGGGGTAGGGGGTAGGGGGTAGGGGGTAGGGGGG	?	2575 GACCCGGCCGGCGACGTAGCGGGTGGCCCCGGCCAGCCCGGGGAAAACCGGGCCTCCCGGTA 2634	₽ <b>&amp;</b>
S95 GTCGAGCAGCTCGCCGAACCCGGCCGGTCCAGGTCGAACCGACGGCGATCTGCTCCAA	B &	2515 GATGCTGCGGCCCGACGTGACGAAGTCGTGGACGACCGAGTGCAGGCTCCGGGGCTCCGGGGCT 2574	유 성
3535 GTACTIVGCCGGGGCCTGCTCCACCGCCGTGCCCACTGCGGATTGCAACAG 3594	B &	2455 CCGGGCGGTCACCGACTGGTCGAAACCGTCGAGGAAGAACTCGTCCCCCGGCTGCGGATC 2514	유 성
CUCCUGITACUGUAGCUTCAACGUGGCGGCGGTTCACGGCCTGATGCTTCGTTCGT 	) B &	2395 GCGGATCAGGCCCCGATGCTGATCCCACCCGTCGGCGACGTCCCGTTCGAGTTGGTTG	g &
3415 ACAGCGGAACATGCACGTCGGGCCGGGGTAGAGCCCGACGCTGTACGGGAAGGCGGGCCC 3474	) B &	Query Match 14.2%; Score 1269.8; DB 1; Length 15052; Best Local Similarity 66.6%; Pred. No. 3.8e-82; Matches 1940; Conservative 0; Mismatches 907; Indels 66; Gaps 6;	Que Bes Mat
355 719	ДУ	<pre>/gene="ole!" /function="intracellular inactivation of oleandomycin by glycosylation" /codon_start=1</pre>	
3295 GAGGTACATCGCCGTCGGGTTCTCCCGACGGCACCTCGTCGATGACCGGAGGTGAGGATCTC 3354	g Q	BEYFLDGFDQTVTARLNQMETDIADGWAEHRGFLR"  995711231  CDS 995711231	

GG 7640 CC 4434 CC 7586 GC 758	5215 GTCGGGGGCACCGCCGTCGTCGAAGTCCGCGGG 5247	5155 GTTGACGTAGTGGCTGTGCGCGAGGAGCTGGTGGTCGGCGAAGGTCATCCACCGGTG	5095 TCACGCCGTCGCCCGGTTGTAGACGGCGGACGCGCAGGCGACGAGGCTGGACTGGAT	5035 GCAGGGGTGCAGGAACGCCTCGGGACCGCCGAAGATCGCCAGATCGGTCGG	4975 GGGCCACTCCAGGCGGGCCAGGAACCGCTGCCGGTCGCCGATCGTCGGCCGGC	4915 CGACCOGGGCCTCGAACTCCCGCACCAGGGGCCGCCGTTGGTGAGCCAGTTGTTGTTCA	4855 GTTCCAGGGCGACGGTGGCGTTGCAGGTGGCGATGCAGTGCGGTACCCCGACCAGGTCGG	4795 CCGCGAAGGTCATTGACGGCATGATCACTTCACCGGTGACGTCACCGGCCCCGCAGCACCACACACA	4735 CCGGGTCGACGTCGCAGAACACCGGTGTGAGTCCGAGCCAGCTCGCCGCGTGCGCGTGGGCGTGGGCGGTGGGCGGTGGGCGGTGGGCGGGTGGGCGGGGGG	4675 TCGCGCCGGTCTGCGGGGTGACGAGCGCGGCGACGTGGTCCGGGTCGACCAGACCGGTCG	4615 CGGCGATCTTCGCCAGGCGCCTCCACAGGTGGTCGGCCCCACAGGTGTACGCCGACGA	4555 CACCCGTCGTGCAGCCCAGGGCGTGGGCGGCGTCGAAGAAGAGCTTGACCTGGTCGGTC	4495 CCGCCTTGGTGGCGTGGAAGCTGAACACCTCGGCGTCACCGGATCCGCCCACCGGACGTC	4435 GGATCCGTTCGGCCAGCAGGCCGTCGTCGGTGACCACCGCCCCGCCCTCGAAGGCGGTGA	4375 CGTTGGTGCCGATCTCGGTGACCACCTTGTCCGGGCCGATGCCGAAGTTGTGCATGGCCC	
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Search completed: April 7, 2006, 16:58:07 Job time : 43636.7 secs

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Minimum
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Listing first 45 by
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Perfect score:
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, 2006, 02:28:59;
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10.3	10.3	10.3	10.3	10.4	10.7	10.7	10.7	10.7	10.9	11.0	11.1	11.2	11.2	11.3	11.3	11.5	11.8	11.9	11.9	11.9
15872	15872	4411529	4403765	5760	1248	109519	31422	2076	390	33529	1683	4411529	43280	44377	44377	4403765	1881	49377	28958	85682
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US-09-091-609-1	US-09-105-537-1	US-09-103-840A-1	US-09-103-840A-2	US-10-152-886-14	US-09-724-797-23	US-09-758-759-1	US-09-914-286-2	US-09-758-759-78	US-09-197-649-7	US-09-144-085-3	US-09-724-797-21	US-09-103-840A-1	US-08-804-227C-1	US-08-804-198-1	US-08-804-227C-7	US-09-103-840A-2	US-09-434-288-5	US-08-764-233A-1	US-09-028-934-6	US-08-729-214-6
Sequence 1, Appli	Sequence 1, Appli	-	Sequence 2, Appli	Sequence 14, Appl	Sequence 23, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 78, Appl	Sequence 7, Appli	Sequence 3, Appli	Sequence 21, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 6, Appli

ALIGNMENTS

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INAME/KEY: CDS
IOCATION: (1)...(144)

OTHER INFORMATION: megBVI(megT), TDP-4-keto-6-deoxyglucose-2,3-dehydratase;
OTHER INFORMATION: SEQ ID NO: 2= translated amino acid sequence
NAME/KEY: CDS
ILOCATION: (928)...(2061)
OTHER INFORMATION: megDVI, TDP-4-keto-6-deoxyglucose 3,4-isomerase,
OTHER INFORMATION: TDP-4-keto-6-deoxyhexose 3,4-isomerase;
OTHER INFORMATION: SEQ ID NO: 3= translated amino acid sequence
NAME/KEY: CDS
ILOCATION: (2072)...(3382)
OTHER INFORMATION: megDI, rhodosaminyl transferase (eryCIII homolog),
OTHER INFORMATION: TDP-megosamine glycosyltransferase;
OTHER INFORMATION: SEQ ID NO: 4= translated amino acid sequence
NAME/KEY: CDS
ILOCATION: (3462)...(4634)
OTHER INFORMATION: segG(megY), mycarosyl acyltransferase, mycarose O-acyltransf
OTHER INFORMATION: SEQ ID NO: 5= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McDaniel, Robert
APPLICANT: Volchegursky, Yanina
FITTLE OF INVENTION: Recombinant Megalomicin Biosynthetic
FITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 300622004700
CURRENT APPLICATION NUMBER: US/09/679,279
CURRENT FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/158,305
PRIOR APPLICATION NUMBER: US 60/190,024
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 34
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 34
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US-09-679-279-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09679279 Patent No. 6524841 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 1
NAME/KEY: CDS
LOCATION: (4651)...(5775)
LOCATION: (4651)...(5775)
OTHER INFORMATION: megDII, deoxysugar transaminase (eryCI, DnrJ homolog),
OTHER INFORMATION: TDP-3-keto-6-deoxyhexose 3-aminotransaminase;
OTHER INFORMATION: SEQ ID NO: 6= translated amino acid sequence
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Micromonospora megalomicea FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                          mycarose O-acyltransfera
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NAME/KEY: misc feature
LOCATION: (22318)...(22575)
LOCATION: (22318)...(22575)
OTHER INFORMATION: megAI, ACP2
NAME/KEY: CDS
LOCATION: (22867)...(33555)
OTHER INFORMATION: megAII; SBQ ID
NAME/KEY: misc feature
LOCATION: (22957)...(24237)
OTHER INFORMATION: megAII, KS3
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (13849)...(15126)
OTHER INFORMATION: megAI, KS1
NAME/KEY: misc_feature
LOCATION: (15427)...(16476)
OTHER INFORMATION: megAI, AT1
NAME/KEY: misc_feature
LOCATION: (17125)...(17694)
OTHER INFORMATION: megAI, KR1
NAME/KEY: misc_feature
LOCATION: (17947)...(18207)
OTHER INFORMATION: megAI, ACP1
NAME/KEY: misc_feature
LOCATION: (19948)...(19948)
OTHER INFORMATION: megAI, KS2
NAME/KEY: misc_feature
LOCATION: (19876)...(20910)
OTHER INFORMATION: megAI, KS2
NAME/KEY: misc_feature
LOCATION: (19876)...(20910)
OTHER INFORMATION: megAI, AT2
NAME/KEY: misc_feature
LOCATION: (21517)...(22053)
OTHER INFORMATION: megAI, KR2
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: (24544)...(25581)
OTHER INFORMATION: megAII, AT3
NAME/KEY: misc_feature
LOCATION: (26230)...(26733)
OTHER INFORMATION: megAII, KR3 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (8228)...
OTHER INFORMATION: 0
OTHER INFORMATION: 9
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OTHER INFORMATION: megAI, AT-L
NAME/KEY: misc_feature
LOCATION: (13576)...(13791)
OTHER INFORMATION: megAI, ACP-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (12181)...(22821)
OTHER INFORMATION: megAI; SEQ ID NO:
NAME/KEY: misc_feature
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LOCATION: (10483)...(11424)
OTHER INFORMATION: megBIV,
OTHER INFORMATION: TDP-4-ke
OTHER INFORMATION: SEQ ID N
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LOCATION: (9226)...(10479)
OTHER INFORMATION: megBV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: (7220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (8228) ... (9220)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              megBIV, TDP-hexose 4-ketoreductase, TDP-4-keto-6-deoxyhexose 4-ketoredu SEQ ID NO: 12= translated amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               megBV, mycarosyl transferase, mycarose glycosyltransferase; SEQ ID NO: 11= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose 2,3-reductase, SEQ ID NO: 10= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          megDV, TDP-hexose 4-ketoreductase (eryBIV, dnmV TDP-4-keto-6-deoxyhexose 4-ketoreductase; SEQ ID NO NO: 9= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
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D: 7= translated amino acid sequence
                                                                                                                                                                                                                                                    ID NO: 14= translated amino acid sequence
             (inactive)
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i amino acid sequence
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; LOCATION: (47411).
; OTHER INFORMATION: US-09-679-279-1
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 600; Conservative 0
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LOCATION: (28897)...(29931)
OTHER INFORMATION: megAII, AT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (29953)...(30477)
OTHER INFORMATION: megAII, DH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: megAII, ACP3
NAME/KEY: misc feature
LOCATION: (27353)...(28590)
OTHER INFORMATION: megAII, KS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (41406)...(41936)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (39795)...(40811)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (38187)...(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (37860)...(38120)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (37068)...(37604)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (35385)...(36419)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (33780)...(35027)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (33666)...(43271)
OTHER INFORMATION: megAIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (33052)...(33312)
OTHER INFORMATION: megAII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (33052)...(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: megAII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (31396)...(3
                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (43268).
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_fe
LOCATION: (42585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (42168)...(4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (39795)...(4)
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LOCATION: (37860)...(3
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LOCATION: (37068)
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                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                 OCATION:
                                                                                          (47411)...(47980)
NRMATION: megF, C-6
                                                                                                                                             (46660)...(47403)
RMATION: megH, TEII;
                                                                                                                                                                                                                                                                                             (44355)...(45623)
RMATION: megCIII, di
RMATION: SEQ ID NO:
                                                                                                                                                                                                                                                             (45620)...(46591)
                                                                                                                                                                                                                                                                                                                                                                                                         (43268) ... (44344)
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                                                                                                                                                                                                    megBII-2(megBII), TDP-4-keto-6-deoxy-1-glucose TDP-4-keto-6-deoxyglucose 2,3 dehydratase; SEQ ID NO: 18= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                     megCII, TDF
SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ER4
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                                                                                                                                                                                                                                                                                                                                                                       TDP-4-keto-6-deoxyglucose 3,4-isomerase;
NO: 16= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACP5
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D: 17= translated amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                            hydroxylase;
Score 600; DB 3;
Pred. No. 1.3e-102;
Mismatches 0;
                                                                                                                                                   SEQ ID NO: 19=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO: 15= translated amino acid sequence
                                                                                              SEQ
                                                                                                                                                   translated amino acid sequence
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                                     Length 47981;
                                                                                              20= translated amino acid
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Gaps

4952.US.

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COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
TOTOTOTRATION NUMBER: 32652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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US-07-642-734C-3
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APPLICANT: Katz, L
APPLICANT: MCalpine, J
APPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application Patent No. 5824513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: A
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Abbott Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGGCTGGTGACCAGGGACGCCGCCGCCGTGACCGTCGGAGACGACGTCGATCCGGCCC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGCCTGGACACCCTCGCGTTGGTCCAGGCGCTCGGCGCAGCCGGGATCGACGTCCCCC 36786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGCCTGGACACCCTCGCGTTGGTCCAGGCGCTCGGCGCAGCCGGGATCGACGTCCCCC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCCCCGGCCTGGACGGACGTCGTCCGCGACGGCCTGGAACAGCGCGGGGGGGACCGTCG 36606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA Method
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                                                                                                                                                                                                                                                  Version
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REFERENCE/DOCKET NUMBER: 495:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEPAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE: misc_feature NAME/KEY: misc_feature LOCATION: 1693..2670 OTHER INFORMATION: /func OTHER INFORMATION: acyl
NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /func
OTHER INFORMATION: dehyd
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9433..9984
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /func
OTHER INFORMATION: acyl
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /codo
OTHER INFORMATION: /func
OTHER INFORMATION: /prod
OTHER INFORMATION: 6-deo
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19..4470
OTHER INFORMATION: modul
                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 4471..5847
OTHER INFORMATION: /func
OTHER INFORMATION: beta
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 3406..3921 OTHER INFORMATION: /func OTHER INFORMATION: beta-FEATURE:
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NAME/KEY:
LOCATION:
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ORGANISM: Sac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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OTHER
                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 4471..10722
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OTHER INFORMATION: /fur OTHER INFORMATION: beta
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STRAIN: NRRL 238
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                     /KEY: misc_feature
TION: 6054..7026
R INFORMATION: /func
R INFORMATION: acyli
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beta-ketoacylACPsynhase
                                                                                   /function= "approximate span of
dehydratase and enoylreductase
                                                                                                                                                                                                                                                                                                                                          /function=
module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                             acyl carrier
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/product= "eryA ORF2 e
6-deoxyerythronolide B
 /function= "approximate span
beta-ketoreductase of module
                                                                                                                                                                     /function= "approximate acyltransferase domain o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function= "approximate span of
beta-ketoreductase domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "approximate span of beta-ketoacyl ACP synthase of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function=
module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /function= "approximate span
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                                                                                                                                                                                                                                                                                                                                                          "approximate span
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                                                                                                                                                                                                                                                                                                                                                                                                                             domain of module
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                                                                                                                                                                     e span of of module
                                                                                                                                                                                                                                                      span of
domain
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                                                                                     domains
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OTHER INFORMATION
OTHER INFORMATION
FEATURE:

NAME/KEY: misc feature
IOCATION: 14857..15114
OTHER INFORMATION: /func
OTHER INFORMATION: acyl
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LOCATION: misc feature

LOCATION: 15166.20235

OTHER INFORMATION: /function

OTHER INFORMATION: module feature:

NAME/KEY: misc

LOCATION:
Query Match
Best Local Similarity
Matches 420; Conserv
                                                                   -07-642-734C-3
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FEATURE:

NAME/KEY: misc_feature
LOCATION: 10831..12174
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12379..13350
OTHER INFORMATION: /func
OTHER INFORMATION: acylt
FEATURE:
NAME/KEY: misc_feature
LOCATION: 14062..14610
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 15172.16569
OTHER INFORMATION: beta-
PEATURE:
NAME/KEY: misc_feature
LOCATION: 16768.17721
OTHER INFORMATION: func
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NAME/KEY:
LOCATION:
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NAME/KEY: misc feature
LOCATION: 10723..15165
OTHER INFORMATION: /fur
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NAME/KEY:
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                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
                                                                                                                                                                                                                                                 NAME/KBY: misc feature LOCATION: 18379...18921 OTHER INFORMATION: /fur OTHER INFORMATION: beta
                                                                                 NAME/KBY: misc feature LOCATION: 19492..20235 OTHER INFORMATION: /fur OTHER INFORMATION: thic
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TION: 14062..14610
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   Conservative
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                 47.8%;
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acyltransferase domain of modul
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/function= "gene =eryA"
/product= "orf3 encoding modules 5
6-deoxyerythronolide B formatio"
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module 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function=
module 5"
                                                                                  /function= "approximate span of
thioesterase domain of module 6"
                                                                                                                                                                  /function= "approximate span of
acyl carrier domain of module 6"
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acyltransferase domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acyl carrier
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beta-ketoreductase of module
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beta-ketoreductase domain of
                                                                                                                                                                                                                                                                                                                                                                                                                    /function= "approximate span of beta-ketoacylACPsynthase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "approximate span of acyl carrier domain of module 5"
Score 286.6; DB 2; Length 20235; Pred. No. 1.1e-44; 0; Mismatches 174; Indels 9;
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US-08-439-009A-3
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Patent No. 6004787
GENERAL INFORMATION:
ZIP: 60064-3500
COMPUTER RAADABLE FORM:
COMPUTER: RAADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAX-1995
CLASSIFICATION: 435
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STATE: IUS
COUNTRY: US
TTD: 60064-3500
TRADABLE F
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APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  STREET: Abbott Laboratories D37
STREET: Park Rd
CITY: Abbort T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCCACCGGCGGGCGCGCACGGACGACGACGACGACGACCAGGTCGTATGGC 13483
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ATTORNEY/AGENT INFORMATION:

Casuto, Dianne

REGISTRATION NUMBER: 40 REFERENCE/DOCKET NUMBER:

40,943

4952.US.D1

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NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /function= "app
OTHER INFORMATION: acyl carrier do
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4471..10722
OTHER INFORMATION: /function= "app
OTHER INFORMATION: module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 19..10722
OTHER INFORMATION: /c
OTHER INFORMATION: /p
OTHER INFORMATION: /p
OTHER INFORMATION: 6-
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                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
                 FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                        NAME/KEY: misc feature
LOCATION: 7165.9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and enoylreductase
                                                                                                                               NAME/KEY: misc feature LOCATION: 6054..7026 OTHER INFORMATION: /fur OTHER INFORMATION: acyl
                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KBY: misc feature LOCATION: 3406.3921 OTHER INFORMATION: /fur OTHER INFORMATION: beta
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OTHER INFORMATION: /fur OTHER INFORMATION: acyl
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STRAIN: NRRL 238
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4471..5847
misc_feature
9433..9984
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beta-ketoacylACPsynhase domain of module"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function= "approximate span of acyltransferase domain module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function= "approximate span of
beta-ketoacyl ACP synthase of module 3"
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4
6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function= "approximate span of
beta-ketoreductase domain of module
                                                                                                                                 /function= "approximate span of
acyltransferase domain of module
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module 3"
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acyl carrier domain of module 3"
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US-08-439-009A-3
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NAME/KEY: misc feature
LOCATION: 15172..16569
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
                                                                                                                                                                                                    PEATURE:

NAME/KEY: misc feature
LOCATION: 18379..18921
OTHER INFORMATION: /func
OTHER INFORMATION: beta-
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NAME/KEY: misc feature
LOCATION: 10723.15165
OTHER INFORMATION: /func
OTHER INFORMATION: modul
PEATURE:
NAME/KEY: misc feature
LOCATION: 10831.12174
OTHER INFORMATION: beta-
                                                                      FEATURE:
NAME/KEY:
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                                                                                                          NAME/KEY: misc feature LOCATION: 19149..19398 OTHER INFORMATION: /fur OTHER INFORMATION: acyl
                                                                                                                                                                                                                                                                                                   NAME/KBY: misc feature LOCATION: 16768..17721 OTHER INFORMATION: /fur OTHER INFORMATION: acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: 15166..20235 OTHER INFORMATION: /fur OTHER INFORMATION: modu
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LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
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LOCATION:
                 OTHER INFORMATION: OTHER INFORMATION:
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LOCATION: 12379..1330
OTHER INFORMATION: /function= "approximatr span of
OTHER INFORMATION: acyltransferase domain of module
                                                       LOCATION:
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LOCATION: 10225..10483
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
                                                   misc_feature
19492..20235
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10723..20235
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               /function= "approximate span c
thioesterase domain of module
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acyltransferase domain of module
                                                                                                            /function= "approximate span of
acyl carrier domain of module 6"
                                                                                                                                                                                                      /function= "approximate span of
beta-ketoreductase domain of module
                                                                                                                                                                                                                                                                                                                                                                                             /function= "approximate (
beta-ketoacylACPsynthase
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beta-ketoreductase of module
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beta-ketoacylACPsynthase domain of modul"
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/product= "orf3 encoding modules
6-deoxyerythronolide B formatio"
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module 5"
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Query Match Best Local Similarity

47.8%; 69.7%;

Score 286.6; DB 3; Pred. No. 1.1e-44;

Length 20235;

Mon

6

Gaps

13778 304

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Toupet, Christine
APPLICANT: Toupet, Christine
APPLICANT: Engel, Nathalie
ITITLE OF INVENTION: Rifamycin biosynthesis generated the state of the st
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                                                                       ; SEQ ID NO 3
, LENGTH: 53799
; TYPE: DNA
; ORGANISM: Amycolatopsis mediterranei
US-10-042-665A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-10-042-665A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10042665A Patent No. 6924106
Query Match
Best Local
                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccececrceceaeceracacceeeeeeeereeaeerceaereeaecreeceraccecaereeere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTGTGGCTGGTGACCAGGGACGCCGCCGCCGGTGACCGTCGGAGACGACGTCGATCCCGG
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  Score 98;
Pred. No.
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US-07-642-734C-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Macalpine, J
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Exychromycin Analogs
TITLE OF SECULENCES: 27
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Patent No. 582451
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                                                                                                                                                      ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/642,734C

FILING DATE: 17-JAN-91

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                     STATE: -- US
COUNTRY: US
COUNTRY: 60064-3500
TTP: 600ADABLE F
                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
                             REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
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CGATCCGGC

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598 14018

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TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS

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nucleic acid

double

TOPOLOGY: unknown STRANDEDNESS: LENGTH:

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LOCATION: 6678.8066
OTHER INFORMATION: /funct
OTHER INFORMATION: beta-k
FEATURE:
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OTHER INFORMATION: /prod
OTHER INFORMATION: 6-deo
FEATURE:
NAME/KEY: misc_feature
LOCATION: 744.-1868
OTHER INFORMATION: /func
OTHER INFORMATION: acylt
                                                                                                                                                   FEATURE:
NAME/KEY:
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NAME/KEY:
LOCATION:
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NAME/KEY: misc_feature

**COCATION: 744..6659

**TOCATION: 744..6659
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LOCATION: 6678..112
OTHER INFORMATION:
OTHER INFORMATION:
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                                    NAME/KEY: misc_feature
LOCATION: 8262..9305
OTHER INFORMATION: /function= "approximate
OTHER INFORMATION: acyltransferase domain c
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LOCATION: 6369.6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module
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OTHER INFORMATION: /fur
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LOCATION: 2250..3626
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
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LOCATION: 1998...2198
OTHER INFORMATION: /function= "approximate s
OTHER INFORMATION: acyl carrier domain 1 of
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6678..11219
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5574..6125
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misc_feature
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module 2"
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LOCATION: 10707..10964
OTHER INFORMATION: /fur
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AGGCGAAGCTGTGGGGGCTGGGCCAGGTCGCGTCCCTGGAACGCGGGCCCCGCTGG 9743
                             TGTGGCTGGTGACCAGGGACGCCGCCGCCGTGACCGTCGGAGACGACGTCGATCCGGCCC
                                                                                                                           GTGCGGTGCAAACCCTTGTGCTGGTGCGGGAACTCGACGCCGAGGGCATCGACGCGCCAC
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                                                              TGTGGACGGTCACCTTCGGCGCGGTCGACGCG----GGCAGTCCGGTGGCCCGCCCGGACC
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beta-ketoreductase domain of
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Pred. No. 6.3e-09;
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US-08-439-009A-1 Sequence 1, Application Patent No. 6004787

GENERAL INFORMATION: APPLICANT: Donadio, SAPPLICANT: Katz, L
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis
TITLE OF INVENTION: Specific Polyketides
TITLE OF INVENTION: Specific Polyketides NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F. STATE: 1 COUNTRY: STREET: Abbott Laboratories D377/AP6D-2 One STREET: Park Rd CITY: Abbott Park 60064-3500 Application US/08439009A I g Weinstock

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Abbott

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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OTHER INFORMATION: acyltran FEATURE: NAME/KEY: misr Corrections of the correction of
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OTHER INFORMATION: /funct
OTHER INFORMATION: MODULE
OTHER INFORMATION: /label-
FEATURE:
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LOCATION: 744..11219
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feat
LOCATION: 744..1868
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APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Sac
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
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OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 5574..6125
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase domain of
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LOCATION: 2250..3626
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
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LOCATIO: 1998...2118
OTHER INFORMATION: /function= "a
OTHER INFORMATION: acyl carrier
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LOCATION: 6369.6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module
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OTHER INFORMATION:
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LOCATION: 3831..4811
NAME/KEY: misc feature LOCATION: 6678..11219 OTHER INFORMATION: /fur
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/product= ""ORF1 encoding modules 1 & 2 for
6-deoxyerythronolide B""
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beta-ketoacylACP synthase domain/module1"
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acyltransferase 2 domain
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FEATURE:
NAME/KEY: misc feat
LOCATION: 6678.806
OTHER INFORMATION:
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LOCATION: 8262. 9305
OTHER INFORMATION: /function= "approximate
OTHER INFORMATION: acyltransferase domain o
FEATURE:
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LOCATION:
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                                      TOTOGACOGTCACCTTCOGCOCOGTCOACOCO---GCCAGTCCGGTGOCCCCCGGACC
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Pred. No. 6.3e-09;
0; Mismatches 243;
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RESULT 7
US-09-105-537-30
; Sequence 30, Application
; Patent No. 6265202

US/09105537A

GENERAL INFORMATION:

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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
FILE OF INVENTION: DNA encoding methymycin and FILE OF INVENTION: DNA encoding methymycin and CURRENT APPLICATION UNMBER: US/09/105,537A
CURRENT APPLICATION UNMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 30
LENGTH: 13842
Sequence 5, Application U.
Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
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Best Local Sim
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ORGANISM: Streptomyces
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ilarity 52.6%;
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Pred. No. 3.1e-08;
0; Mismatches 271;
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RESULT 9 US-09-320-878-19

Sequence 19, Application Patent No. 6117659 GENERAL INFORMATION:

US/09320878A

APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINA

O

INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE

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; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; EQ ID NO 5
; LENGTH: 36778
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
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Best Local Similarity 52.6%;
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                                                                 CCGACCGGGCCATGCTCTGGGGCCTCGGCGCGTCGCCCTTGAGCACCCCGAACGCT
                                                                                         CCCTGTGGCTGGTGACCAGGGACGCCGCCGCCGTGACCG---TCGGAGACGACGTCGATC
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Pred. No. 3e-08;
0; Mismatches 271;
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FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/10,880
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
EARLIER EPILING DATE: 1998-05-28
NUMBER: DATE: 1998-05-28
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SEQ ID NO 19
LENGTH: 38506
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Best Local Similarity
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TYPE: DNA
ORGANISM: Streptomyces venezuelae
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CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER APPLICATION NUMBER: PROV. 60/087,080
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
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Best Local S
Matches 317
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APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Sin hes 317;
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llarity 52.6%;
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Pred. No. 3e-08;
0; Mismatches 271;
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APPLICANT: ASSILEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
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; ORGANISM: Streptomyces venezuelae
US-09-657-440-19
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US-09-657-440-19
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SEQ ID NO 19
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                                                                                                                    ACGGACTCGTACCGCAGGTCGCCTGGGTCCAGGCGCTCGGCGACGCCGGAATCAAGGCGC
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 09/657,440
PRIOR FILING DATE: 2000-09-07
PRIOR PRIOR DATE: 1090-05-27
PRIOR PPLICATION NUMBER: US 09/141,908
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: US 09/073,538
PRIOR APPLICATION NUMBER: US 08/846,247
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US-09-793-708-19
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US-09-793-708-19
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SOFTWARE: PatentIn Ver. 3
SEQ ID NO 19
LENGTH: 38506
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APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Me
APPLICANT: BETLACH, Ma
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6086 --- CCCGGCTCACCGCACTGACGACCGGTGACGGCTTCACCGGCGTGGTCTCGCTCCTCG
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BETLACH, Mary C.
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Pred. No. 3e-08;
0; Mismatches 271; Indels 15;
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; TYPB: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-34
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US-09-105-537-34
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APPLICANT: Liu, H.
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Best Local Similarity 53.5%;
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APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycir
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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CCCCGCCCGGTGGG
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                                                         CGACGTCGATCCGGCCCAGGCCATGGTCGGTCGGTCGGCCTGGGCCTGGAGTC 583
                                                                                                        GATCGACGTCCCCCTGTGGCTGGTGACCAGGGACGC---CGCCGCCGTGACCGTCGGAGA
                                                                                                                                               CTCGCTCCTCGACGACCTCGTGCCACAGGTCGCCTGGGTGCAGGCACTCGGCGACGCCGG
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                                         CCCCGCCGACCCGACCGGGCCATGCTCTGGGGCCTCGGCCGTCGTCGCCCTTGAGCA 3152
                                                                                            AATCAAGGCGCCCCTGTGGTCCGTCACCCAGGGCGCGCGTCTCCGTCGGACGTCTCGACAC
                                                                                                                                                               CCCCAGCCTGGACACCC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 187;
                                                                                                                                                                 TICGCGTTGGTCCAGGCGCTCGGCGCAGCCGG
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GENERAL INFORMATION:
APPLICANT: KOSAN BIOSCIENCES,
APPLICANT: REEVES, CHRISTOPHI
APPLICANT: CHU, DANIEL
                                                     Sequence 1, Application Patent No. 6503737
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
FILE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US;
CURRENT APPLICATION NUMBER: US/09/105,537A;
CURRENT APPLICATION NUMBER: US/09/105,537A;
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASUSEQ for Windows Version 3.0;
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-105-537-32
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Best Local Similarity 49.8%;
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TYPE: DNA
ORGANISM: Streptomyces
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AGGCCATGGTGTGGGGCATGGGCCGGGTCGCCCTGGAGCACCCCGAGCGGTGGGGCG
                      GGCTGGTGACCAGGGACGCCGCCGCCGTGACCGTCGGAGACGACGT---CGATCCGGCCC
                                                                                                                                                         CCGGCGCCACCCTCACCCTGGTGCAGGCGCTGGAGGACGCCGGCGTCGCCGCCGCTGT
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Pred. No. 3.1e-07;
0; Mismatches 265;
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CHRISTOPHER

US/09410551E

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APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20026.00
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR APPLICATION NUMBER: US 60/123,748
PRIOR APPLICATION NUMBER: US 60/102,748
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-5518-1
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Best Local Similarity 48.6%;
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                      54958 AACTCGTCATCGAGACGCCGCTCGTGCTGCCGGCGACCGGCGGTGTGGCGGTCTCCGTCG
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GenCore version 5.1.7
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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GenEmbl:*
1: gb ba:*
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98	0.0	100.2	03.2	03.2	124	124	.37.6	189	242	269.2	286.6	286.6	286.6	.86.6	600	600	Score	
16.3	16.7	16.7	17.2					31.5	40.3	44.9	47.8	47.8	47.8	47.8	100.0	100.0	Query	æ
53789	F0285T	11238	125401	123580	60196	4725	210614	31531	9769	20444	32299	20235	20235	20235	47981	47981	Query Match Length DB	
o ⊢	بر د	۰ م	0	μ	σ	σ	بر	11	۳	ب	H	σ	σ	μ	σ	ب	BB	
A69720	AY310323	AX697991	AX211739	AF263912	AX697977	AX697993	AB088224	AY771999	SEERYA	SEERYABS	AY661566	AR095529	AR049368	SERERYAB	AX112026	AF263245	ID	
A69720 Seguence 3	AY310323 Streptomy			AF263912 Streptomy	AX697977 Sequence	AX697993 Sequence	AB088224 Streptomy	AY771999 Synthetic	X56107 S. erythrae	X62569 S.erythraea	AY661566 Saccharop	AR095529 Sequence	AR049368 Sequence	M63677 S.erythraea	AX112026 Sequence	AF263245 Micromono	Description	

## ALIGNMENTS

CDS		qene		source	FEATURES	JOURNAL ?			JOURNAL	i i	AUTHORS	REFERENCE	ORGANISM	SOURCE	VERSION	DEFINITION	Locus	RESULT 1 AF263245
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gene
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LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                     RESULT 2
AX112026
REFERENCE
                                                                                                                            EYWORDS
                                                                                                                                                    VERSION
                                                                        ORGANISM
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Best Local Similarity
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Sequence 1
AX112026
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Micromonospora megalomicea
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Micromonosporineae; Micromonosporaceae; Micromonospora.
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translated amino acid sequence"
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transferase (eryCIII homolog), TDP-megosamine
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TDP-4-keto-6-deoxyglucose-2,3-dehydratase; SI
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NO: 8= translated amino acid sequence"
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TDP-4-keto-1-6-deoxy-hexose 2,3-reductase; SEQ ID I
translated amino acid sequence"
                                                                                                                                translated amino acid
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                                                                                                                             mycarose glycosyltransferase; SEQ ID NO: mino acid sequence"
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LLLERLSDARRHGHPVLAVIRGTAVNSDGASNGLSAPNGRAQVRVIRQALAESGLTPH

100.0%;

Score 600; DB 6 Pred. No. 3e-47;

6, 0

Length 47981; Indels

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Gaps

Mismatches

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/note="unnamed protein product; megBIV, TDP-hexose
/note="unnamed protein product; megBIV, TDP-hexose
/-keotreductase, TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SEQ ID NO: 12= translated amino acid sequence"
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/transl_teble=11
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LPAIYGHSGPGQTGRGVVTAMIRRALAGEPITMMHEGSVRRULHVEDVATAFTAAL
HNHEALVGDVWTPSADEARPLGEIFETVAASVARQTGNPAVPVSVPPPENAEANDFR
SDDPDSTEFRTLTGWHPRVPLAEGIDRTVAALISTKE"
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fdrsyhttrilfyngssvvpqhltsboyrrvcftgsysalgiisnpqefiltlar
fdgeivvtrsgldpasvpdnvrlvdfvpmnillpgcaavihhggagsmatalhhgvpq
isvahewdcylrgqrtaelgagvflrdedvdadtlwqalatvvedrshaenaexlrqe
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AGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG 120
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TGTTGTGCACCGCGAGTCGCGCGCGCCGGATCGGCGCCGCCACTCGACGCCGTCGACGGCA
                                                                                                                                                      TACCCCCGGCCTGGACGGACGTGGTCCGCGACGGCCTGGAACAGCGCGGGGGGCGACCGTCG
                                                                                                                                                                                                      ccercaaccrceecerccrcecreecesaceserccreereereaccescae
                                                                                                                                                                                                                                                        CCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTGGTGGTGACCGGAGCGGCAG
                                                                                                                                                                                                                                                                                                                                                          TCCCCTGGGCCGGGTCCCCGACACCGCGACGACGACGTGGCGTTACCAGCTCGCCTGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                            AGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG
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SERERYAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetal Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharopolyspora erythraea
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beta_ketoacyl-ACP synthase I; beta-ketoreductase; dehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M63677.1 GI:152693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGCTGGTGACCAGGGACGCCGCCGCCGCCGTCGAGACGACGACGACGTCGATCCGGCCC
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                                                                                                                                                                                                                                 translation="MTDSEKVABYLRRATIDIRAARQRIRELESDPIAIVSMACRIPG
GVNTPGMINT | TABLESDPIAIVSMACRIPG
GVNTPGMINT | TABLESDPIAIVSMACRIPG
GVNTPGMINT | TABLESDPIAIVSMACRIPG
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GESSMAVVGGAAVMATFGVFVDFSRQRALAADGRSKARKAGAADGAESCGLEFGDVDAV
LSEARRNGHEVLAVVRASGALVGOSTAGALVGOSTAGALVGOSTAGALVGVTGLIKVVUL
EAHGTGTALGDPIEANALLDTYGRDRDADRPLWIGSVKSNIGHTQAAAGVTGLIKVVUL
EAHGTGTALGDPIEANALLDTYGRDRDADRPLWIGSVKSNIGHTQAAAGVTGLIKVVUL
                                                                VLFAVMVSLAELWRSYGVEPAAVVGHSQGEIAAAHVAGALTLEDAAKLVVGRSRLMRS
LSGEGGMAAVALGEAAVRERLRPWQDRLSVAAVNGPRSVVVVSGEPGALRAFSEDCAAE
GIRVRDIDVDYASHSPQIERVREELLETTGDIAPRPARVTFHSTVESRSMDGTELDAR
                                                                                                                                   ALRNOSLPATIHVEBETPHYUWSSGGVÄLLAGNQPWRRGERTRRÄRVSAFGISGTNAH
VIVEBAPEREHRETTAHDGRPVFLYVSARTTAALRAGNAQIAELLERPDADLAGVGVGLG
LATTRARHEHRAAVVASTREBAVRGLERIAGAATADAVVEGVTEVDGRWNVFFLEPGG
GSQWAGMGABILLSSSFVFAGKIRACDESMAPMQDWKVSDVLRQAPGAPGLDRVDVVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source text: Saccharopolyspora erythraea DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Saccharopolyspora erythraea"
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                                          YWYRNLRETVRFADAVTRLAESGYDAFIEVSPHPVVVQAVEEAVEEADGAEDAVVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA26494.1"
/db_xref="GI:152694"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="eryA"
19. .10722
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of eryA gene,
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misc\_feature

/note="putative" /function="'approximate 4471, .5847

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module

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module

1471. .10722 'gene="eryA"

function="'approximate

span

of acyl carrier domain of

note="putative"

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of module 3, 4171. .4428 /gene="eryA"

function="'approximate span of beta-ketoreductase of module 3, possibly non-functional'"

domain

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module 3'"

'gene="eryA"

note="putative"

function="'approximate span

of acyltransferase domain of

misc\_feature

1693. .2670

/gene="eryA"

note="putative"

/note="putative"
/function="'approximate
of module 3'"

span of beta-ketoacyl ACP synthase

/gene="eryA"

/note="putative" /function="'approximate

apan

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module

/gene="eryA"

misc\_feature

misc\_feature

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PPGGGAQWVCMARADLLESSEV PAESMAS CAEALSPHTDWKLLDVVRGDGGED PHERVD
VLQPYLFSIRVSLAELMRAHGYTPAAVVGHSGGEI AAAHVYAGALSLEBAAAKVVALRSQ
VLRELDDGGGMVSVGASRDELETVLARWDGRVAVAAVNGPGTS VVAGPTAELDEFFAE
AEAREMKPREI AVRYASHSPEVAR I EDRLAAELGTI TAVRGSVELHSTYTGSV IDTSA
MDAS YWYRNLRR PVLFEQAVRGLVEGGEDTFVEVS PHEVLLMAVESTTAEHAGAEVTCV
PTLRREQSGPHEFLRALLLAAHVHGVGADLLFRAVAGGFPAELFTYPFEHQRFWPREPHRP
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ALRAAWRKDDSVYAEVSI AADEEGYAFHPULLDAVAGTLSGLEDGAVTLYR SEPEGDDRAAA
DLADAQWSQHATGTIAAGGVAAGFDTGWFPEDAVRI VRSTGEKWEQPEPRAG
EGELHALDWGRLAEFGSTGRVVAADASDLDAVLRSGEPEDAVLVYR YEBEGDDRRAAA
RHGYLWAAALVRRHEEQEELFGATLV I ATSGAVTVSDDDS VPBEGAAAMWGVI RCAQA
ESPDRFVLLDTDAEFGMLPAVPDNPQLALRGDVFPRLSFLAABSALTLEAGTGRAVP
GDGAI DSVAFEPAADVPGDLAAGEVRVDVARTGVNPRDVLLALGWYPGKADMGTERAG
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VVTAVGPDVDAFAFADDVSQALAAGGTURATGVNRADAAAVPI IAYT
AHYALHDLAGGERAGGSVLI HAAAGGVGWAAVALARRAGAEVLATTAGPAKHGTLRALGL
DDEHI ASSRETGFARKFRERTGGRGVDVVLMSLTGELLDSSADLLAGDGVFVEMGKTD
DDEHI ASSRETGFARKFRERTGGRGVDVVLMSLTGELLDSSADLLAGDGVFVEMGKTD
DDEHI ASSRETGFARKFRERTGGRGVDVVLMSLTGELLDSSADLLAGDVFVEMGKTD
DDEHI ASSRETGFARKFRERTGGRGVDVVLMSLTGELLDSSADLLAGDVFVEMGKTD
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                                                   SDQVAGLAELVRSHAAAVSGYGSADQLPERKAFKDLGFDSLAAVELRNRLGTATGVRL
PSTLVFDHPTPLAVAEHLRDRLFAASPAVDIGDRLDELEKALEALSAEDGHDDVGQRL
                                                                                                                                                                                                                                                SLNALAALRTTRGLPAKALGWGLWAQASEMTSGLGDRIARTGVAALPTERALALPDSA
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RKRLSASTGLRLPASLVFDHPTVTALAQHLRARLVGDADQAAVRVVGAADESEPIAIV
GIGCRPPGGIGSPEQLMRVLAEGANLTTGFPADRGWDIGRLYHPDPDNPGTSYVDKGG
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GMAAYAAGSAYLDALAEHHRARGRSCTSVAWTPWALPGGAVDDGYLRERGLRSLSADR
AMRTWERVLAAGPVSVAVADVDWPVLSEGFAATRPTALFAELAGRGGQAEAEPDSGPT
ESLLRRWNSRRADAPSTSAISEDASDDELFSMLDQRFGGGEDL'
                                                                                                                                                                                                                                                                                                                 VTSIDEPAVEQVLRAKVDAAWNLHELTANTGLSFFVLFSSAASVLAGPGQGVYAAANB
                                                                                                                                                                                                                                                                                                                                                                     HMSRGRHVGKLVLTQPAPVDPDGTVLITGGTGTLGRLLARHLVTEHGVRHLLLVSRRG
ADAPGSDELRAEIEDLGASABIAACDTADRDALSALLDGLPRPLTGVVHAAGVLADGL
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HLAMQALRRGECSLALAGGVTVMSDPYTFVDFSTQRGLASDGRCKAFSARADGFALSE
                                                                                                                                                                                     lrrggevvfplsinrsalrraefvpevlrgmvraklraagqaeaagpnvvdrlagrse
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RYQVWAREASWESASILAGAVILIVTEGGYPSELSDAIRSCLEQSGATVLTCDVESRSTI
GTALEAADTDALSTVYSLLSRDGEAVUPSLDALALVQALGAAGVEAPLAVLTENAVQV
ADGELVDPAQAAVGGLGRVVGIEQPGRWGLVDLVDAIRSLASVLAABRAVLADPREGQV
AIRADGIKVARLVPAPARAARTRWSPRGTVLVTGGTGGIGAHVARWLARSGAEHLVLL
GRRGADAPGASSLREBLTALGTGVTIAACDVADRARLBAVLAABRAEGRTVSAVMHAA
GVSTSTPLDDLTEABFTEIADVKVRGTVNLDBLCPDLDAPVLFSSNAGVWGSPGLASY
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MARDILLRESQVEADS I RDCERALAPHVDWSITDLLSGARFILRRVDVVQPALFAVMVSI
AALMRSHGVEEPAVVGHSQGEI AAAHVAGALTILEDAAKLVAVESRVLARLIGGQGGAAS
PGLGTEQAABRI GRPAGALS I ASVNGBRS VVVAGESGGPLDELI AECEBAEGI TRARI I PV
DYASHS PQVESI.REBLLITELAGI S PVSADVISTTTGGP I II I AECEBAEGI TRARI I PV
DYASHS PQVESI.REBLLITELAGI S PVSADVISTTTGOF I II I ATMTI TAYVIANILREQ
VRFQDATROLAEAGFDAFVEVSPHVLITVGI BATILDSALPADAGACVVGTILREDGGDI
ADFHTALGEAYAQGVEVDMSPAFADARFVELFYPPEDRORYNILP I PTGGRARGEDDDM
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GTGTRIGDFISVHALLSTYGARRDPDDFLMIGSVORNIGHTQAAAGVAGVMKAVLALR
HGEMPRTLHDDEBSPQIEMDLGAVSVVSQARSWPAGERPRRAGVSSFGISGTNAHVIV
EEAPEADEPEPAPDSGFVFLVLSGRDEQAMRAQAGRLADHLAREPRNSLRDTGFTLAT
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FGISPREALAMDPQQRIMLEISWEALERAGHDPVSLRGSATGVFTGVGTVDYGPRPDE
APDEVLGYVGTGTASSVASGRVAYCLGLEGPAMTVDTACSSGLTALHLAMESLRRDEC
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VFVF PCQGAQWEGMARGILSVPVFAES I AECDAVLSEVAGFSASEVLEQRPDAPSLER
VDVVQPVLFSVMVSLARLMGACGVSPSAVIGHSQGE I AAVVAGVLSIEDGVRVALR
AKALRALAGKGGMVSLAAPGBRARAL I AFWEDN I SVAAVNSPSSVVVSGDPALLAELV
ARCEDEGVRAKTLPVDYASHSRHVEEI RETILADLOGI SARRAAI PLYSTLHGERRDG
ADMGPRYMYDNLRSQVRFDEAVSAAVADGHATTVEMS PHPVLTAAVQEI AADAVAI GS
LHRDTAEEHL I AELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYMLAPEVSDQL
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Sequence 3 from patent US 5824513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGCGCTCGCCGAGGCGTACACCCCGGGGGGTGGAGGTCGACTGGCGTACCGCAGTGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACCGCCCTGTCCACTGTGGTCTCTCTGCTCGCGCTGCCGAGGGCGGTGCTGTCGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCCGTCGACCTCGGGGGGTCCTCCCTGGCCGGACGGGTCCTGGTGGTGACCGGAGCGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTGTGGCTGGTGACCAGGGACGCCGCCGCCGTGGACCGTCGGAGACGACGTCGATCCGG 537
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                                                                                                                                            /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:6005407
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Pred. No. 2.2e-18;
0; Mismatches 174;
      Score 286.6; DB 6;
Pred. No. 2.2e-18;
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Db 138  RESULT 5  AR095529  LOCUS  DEFINITION  ACCESSION  VERSION  VERSION  VERSION  VERSION  VERSION  FEFERENCE  AUTHORS  TITLE  JOURNAL  FEATURES  SOUTCE  ORIGIN  ORIGIN  Query Matches  Gy  Db 133	\$ B	& & &	Db QQ	Db Qq	유 성	B 8	β <b>Q</b>	B 8	B &	da Vy
SULT 5 095529 095529 20235 bp DNA linear PAT 08-SEP-2000 CRESTON AR095529	13838 CGCAGGCCATGGTGGGCGGGTCGGCATCGAGCAGCCGGGGCGCGGGGC13897 598 GTG 600	478 CCCTGTGGCTGGTGACCAGGACGCCGCCGCGTGACCGTCGAGACGACGACGACGACGACGACGCGG 537	418 ACCCCAGCCTGGACACCCTCGCGTTGGTCCAGGCGCTCGGCGAGCCGGGATCGACGTCC 477	358 GCACCGCCTGTCCACTGTGGTCTCTGCTCGGGGCTCGGCCGAGGGGGGGTGCTGTCGACG 417	298 TCGTGTTGTGCACCGCGCAGTCGCGCGCGGATCGGCGCCGCACTCGACGCCGTCGACG 357	238 CAGTACCCCCGGCCTGGACGGGCTGCGACGGCCTGGAACAGCGCGGGGGGGG	178 ACCCCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTGGTGGTGACCGGAGCGG 237	121 TCCCCCTGGGCCGGGTCCCCGACACCCGGCGACGACGACTGGCGTTACCAGCTCGCCTGGC 177	61 AGGGACGCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG 120	1 CCGCGCTCGCCGAGGCGTACACCCGGGGGGTCGAGGTCGACTGGCGTACCGCAGTGGGTG 60
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AY661566 LOCUS DEFINITION ACCESSION VERSION VERSION KEYMORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE GOURNAL REFERENCE AUTHORS TITLE GOURNAL FEATURES GOURCE CDS	Db	8 8	8 8	B 8	용 성	유 성	B &	A A	Q Qy	B &

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          ATCCGTCGCTGGACGCGCTCGCCCTGGTCCAGGCCCTCGGAGCGGCCGGGGTCGAAGCAC
                                                                                                                                                                                                                                                                                                                                                                      ACCCCAGCCTGGACACCCTCGCGTTGGTCCAGGCGCTCGGCGCAGCCGGGATCGACGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAAGCCGAGTGGGAGAGCGCTTCGCTGGCCGGACGCGTGCTGCTGACCGGACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCCCACCGGCGGGCGCACGGACGACGACGACGACTGGCGCTACCAGGTCGTATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCGCGGCCGGTCGAGCTGCCCGTCTACCCGTTCCAGCGGCAGCGGTACTGGCTGCCCA
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                                                                                                                           CGCTGTGGGTGCTGACCCCGCAACGCCGTGCAGGTGGCCGACGGCGAACTGGTCGATCCGG
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                                                                  CGCAGGCCATGGTGGGCGGTCTCGGCCGCGTGGTCGAGCAGCCCGGGGGCGCTGGG
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GTGTELGDE IEVHALLSTYGARRDPDDPLMIGSVVSNIGHTQARAGVRAGDVDYVEAH
GTGTELGDE IEVHALLSTYGARRDPDDPLMIGSVVSNIGHTQARAGVRAGVKAVLALR
HGEMPETLHDEES POL EMDLGAVSVVSQARSWPAGEBRERRAGVSS FGI GSTNAHVIV
EBAPEADEPEPAPDSGPVPLVLSGRDEQAMRAQAGRLADHLARBERNSLEDTGFTLAT
RRSAMEHRAVVVGDRDDALAGLRAVADGRIADRTATGQARTRAGVAMVEPGQGAQMQ
MARDLLREGQVPADSI HDCERALAPHVMSLITDLLSGARPLDRVDVVQPALFAVMVSL
AALWRSHGVEPAAVVGHSQGE IAAAHVAGALTLEDAAKLVAVRSRVLRRLGQQGMAS
FGLGTEQAARBI IGRPAGALSI AASVNGPRSVVVAGESGPLDELI ARCEAEGI TARRI PV
DYASHS PQUESLREELLTELAGI SPVSADVALVSTTTTGQPI DTATMDTAVWYANLREQ
VRFQDATRQLABGAFDARVEVSHPVLTVGI EATILDSALPADAGACVGTLREDDDM
RYQVVWREABWESASLAGRVLLVTGPGVPSELSDAI ENGLEQGGATVLTCDVESRSTI
GTALERADTDALSTVSILLSRDGEAVDPSLDALALVQALGAAGVBAPLWTLTRUNYQV
ADGELVDPAQAMVGGLGRVVGI EQPGRWGGLI DI UDADAAS IRSLAAVLADPRGEEQV
ADGELVDPAQAMVGGLGRVVGI EQPGRWGGLI DI UDADAAS IRSLAAVLADPRGEEQV
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APDEVLGYVGTGTASSVASGRVAYCLGLEGPAMTVDTACSSGLTALHLAMESLRRDEC
GLALAGGVTVMSSPGAFTEFRSQGGLAADGRCKPFSKAADGFGLAEGAGVLVLQRLSA
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/protein_id="AAV51822.1"
/db_xref="GI:55419417"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MSGDNGMTEEKLRRYLKRTVTELDSVTARLREVEHRAGEPIAIV/
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/transi_table=11
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Pred. No. 1.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6-deoxyerythronolide B synthase; acyl carrier protein; acyltransferase; beta-ketoacyl synthase; dehydratase; enoyl reductase; ketoreductase; multifunctional subunits; thioesterase. Saccharopolyspora erythraea Saccharopolyspora erythraea Saccharopolyspora erythraea Bacteria; Actinobacteria; Actinobacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multifunctional enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X62569.1
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X62569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEERYABS
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                                            ALRINGELPATLHVEEPTPHVDWSSGGVALLAGNOPWRRGERTRRÂAVSAFGI SGTINAH
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13337

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CCGCGCTCGCCGAGGCGTACACCCCGGGGGGTGGAGGTCGACTGGCGTACCGCAGTGGGTG

Score 269.2; DB 1; Pred. No. 8.5e-17; 0; Mismatches 183;

Length 20444; Indels 9;

9; Gaps

N س

13396

Query Match Best Local Si Matches 408;

Similarity

44.9%;

Conservative

misc\_feature

8

121 TCCCCCTGGGCCGGGTCCCCGACACGCGACGACGAGGGGGGGTTACCAGCTCGCCTGGCACC 180

ACGCGCGGCCGGTCGAGCTGCCGGTCTACCCGTTCCAGCG---GTACTGGCCTGCCCATCC 13453

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JOURNAL
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AUTHORS
TITLE
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ORGANISM
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TITLE
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Saccharopolyspora erythraea
Saccharopolyspora erythraea
Saccharopolyspora erythraea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Actinobacteridae; Saccharopolyspora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cortes, J., Haydock, S.F., Roberts, G.A., Bevitt, D.J. and Leadlay, An unusually large multifunctional polypeptide in the erythromycin-producing polyketide synthase of Saccharopolyspora
                                                                                                                                                                                                                                                                                                                        Submitted (24-SEP-1990) Leadlay P.F.,
University of Cambridge, Tennis Court
Location/Qualifiers
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Cambridge CB2 1QW,
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ENDERQAMVGLGRVNGLETPENGGGLVDLPALBQFOREAFVACLGADGHEDOVAL
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ORIGIN ب Similarity /gene="eryA" /product="6-deoxyerythronolide B synthase"

mat\_peptide

S 닭 Ś 밁 S Matches 409; Query Match Best Local S 2698 2638 121 61 TCCCCCTG-CCGCGCTCGCCGAGGCGTACACCCCGGGGGGGTGGAGGTCGACTGGCGTACCGCAGTGGGTG ACGCGCGGCCGGTCGAGCCGTCTACCCGTTCCAGCGCGAGCTGCCCGTCTACCCCGT 2757 AGGGACGCCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG 120 CCGCGCTCGGCGAGGCGTACGCGCAGGGCGTGGAGGTCGACTGGAGCCCCGCCTTCGCCG Conservative 40.3%; 0 Score 242; DB 1; Pred. No. 3.5e-14; Mismatches 185; Geccegerccccgacacccgcc Length 9769; Indels 36; Сарв 2697 150 60

gene

RBS

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JOURNAL
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
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DEFINITION
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AY771999
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Synthetic construct DEBS polyketide
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                                                                                                                                                                                                                                                                        Reid, R.C., Kodumal, S.J., Patel, K.G.,
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                                                                                                                                                                                                                                                                                                                    polyketide synthase gene cluster
Natl. Acad. Sci. U.S.A. 101 (44), 15573-15578
                                                                                                                                                                                                                                                                                                                                                synthesis of long DNA sequences: Synthesis of a contiguous
                                                                                                                                                                                                                                           Submission
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                                                                                                                                                                                           CA 94545, USA
Location/Qualifiers
                                                                        notes constructed for expression EryAI, EryAII and EryAIII (DEBSI, three subunits of the polyketide erythromycin biosynthetic cluster
                                                           erythraea"
                                                                                                                                    /mol_type="other DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                   1. .31531
/note="lac operator"
                             'note="T7 promoter"
                                                                                                                                                                 organism="synthetic construct"
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                                                                        in Escherhichia coli of DEBS2 and DEBS3), the synthase from the of Saccharopolyspora
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| Typense="stylat (morphed)"
| Typense="styla
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CDS RBS

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misc_feature
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VLFAVWYSLAELWRSYGYEPAAVVGHSQŒI AAAHVAGALTLEDAKLVVGRSRLWRS
LSGEGGWAAVALGEAAVREERLEWDDLLSVAAVWGFRSVVVSGEPGALRAFSEDCAE
GIRVRDIDVDYASHSPQIERVREELLETTGDIAPRARVTFHSTVESRSWDGTELDAR
YYRNLAETVREADAVTRLAESGYDAFIEVSHPVVVQAVEEADGAEDAVVVGS
LHRDGGDLSAFLRSWATHVSGVDIRWDVALPGAAPFALPTEPQRKRYWLDAPAAPAA
ASDELATRVSWTPIEKESGNLDGDWLVVTPLISPEWTENLCBAINAWGGRALRCAPAA
ASDELATRVSWTPIEKESGNLDGDWLVTTPLISPEWTENLCBAINAWGGAALGARQAPAA
TSASRTEMAQAVQAGTGFRGVLSLLSSDESACKPGVPAGAGLLTIVQALGDAGVDA
TSASRTEMAQAVQAGTGFRGVLSLLSSDESACKPGVPAGAVGLLTIVQALGDAGVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSGTNAHVIVEEAPAEQEAARTERGPLPFVLSGRSEAVVAAQARALAEHLRDTPELGL
TDAAWTLATGRARFDVRAAVLGDDRAGVCAELDALAEGRPSADAVAPVTSAPRKPVLV
PPGQGAQWVGMARDLLESSEVFAESMSRCAEALSPHTDWKLLDVVRGDGGPDPHERVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLAMQALERGECSLALLAGGVTVMSDPYTFVDFSTQRGLASDGRCKAFSARADGFALSE
GVAALVLEELSRARANGHQVLAVLRGSANNQDCASUGLAARUGSQCERVLRQALLASG
VPAADVDVVEAHGTGTELGDPTEAGALLATYGQDDRDELLGSVXTNICHTQAALGAS
GVIKVVLAMRHGMLPRSLHADELSPHIDMESGAVEVLREEVPWPAGERPRRAGVSSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMAAYAAGSAYLDALAEHHRARGRSCTSVAWTPWALPGGAVDDGYLRERGLRSLSADR
AMRTWERVLAAGPVSVAVADVDWPVLSSGPAATRETALFAELAGRGGQAEAEPDSGPT
GEPAQRLAGISEPDEQOENLLEILVANAVAEVLGHESAAEINVRRAFSELGLDSLAWAND
RKRLSASTGLRLPASLVPDHPTVTALAQHLRARLSSDADQAAVRVVGAADESEPIAIV
                                                                                                                                              DLADAQWSQHATGTLAQGVAAGPRDTEQWPPEDAVRIPLDDHYDGLAEQGYEYGPSFQ
ALRAAWRKDDSVYAEVSIAADEEGYAFHPVLLDAVAQTLSLGALGEPGGGKLPFAWNT
VTLHASGATSVRVVATPAGADAMALRVTDPAGHLVATVDSLVVRSTGEKWEQPEPRGG
                                                                                                                                                                                                                                                                                            PTLRREQSGPHEFLRNLLRAHVHGVGADLRPAVAGGRPAELPTYPFEHQRFWPRPHRP
ADVSALGVRGAEHPLLLAAVDVPGHGGAVFTGRLSTDEQPWLAEHVVGGRTLVPGSVL
VDLALAAGEDVGLPVLEELVLQRPLVLAGAGALLRWSVGAPDESGRRTIDVHAAEDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ULQPVI_FSIMVSI.ABI.WRAHGVTPAA.VVGHSQGEIAAAHVAGAI.SI.BAAAKVVAI.RSQ
VLRELDGGGWVSVGASRDBI.ETVIAARWDGRVAVAAKVRGPTS VVAGPTABI.DBEFAB
ABAAEMKPRI AVRXASHSPEVAR I BDRI.ABAILGTI TAVRGSVPLHSTYTGEVI.DTSA
ABAAEMKPRI AVRXASHSPEVAR I BDRI.ABAILGTI TAVRGSVPLHSTYTGEVI.DTSA
MDASYWYRNI.RRPVI.FEQAVRGI.VEQGFDTFVEVSPHPVI.LMAVEETAEHAGAEVTCV
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FLTDAADFDPGFFGITPREALAMDPQQRLMLETAWEAVERAGIDPDALRGTDTGVFVG
MNGQSYMQLLAGEAERVDGYQGLGNSASVLSGRIAYTFGWEGPALTVDTACSSSLVGI
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LVAVLRGGGRAEDHLAVRDGRLHGRRVVRASLPQSGSRSWTPHGVVLVTGAASPVGDQ
LVAVLRGGGRAEDHLAAVEDEAGASAVVCADDAALREALGDEPVTALV
LVRWLADRGABRELVLAGACPGDDLAAVEEAGASAVVCADDAALREALGDEPVTALV
HAGTLTNFGSISEVAPEEFAETIAAKTALLAVLDEVLGDRAVEREVYCSSVAGIWGGA
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VIVEBAPEREHRETTAHDGRPVPLVVSARSTAALRAQAAQIAELLERPDADLAGVGLG
LATTRARHEHRAAVVASTREEAVRGLREIAAGAATADAVVEGVTEVDGRNVVFLFPGQ
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GESSMAVVGGAAVMATPGVFVDFSRQRALAADGRSKAFGAGADGFGFSEGVTLVLLER
LSEARRNGHEVLAVVRGSALNQDGASNGLSAPSGPAQRRVIRQALESCGLEPGDVDAV
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GVNTPQRLWELLREGGETLSGFPTDRGWDLARLHHPDPDNPGTSYVDKGGFLDDAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="eryAII (morphed)"
/note="similar to Saccharopolyspora erythraea EryAII of
GenBank Accession Number AY661566; contains His-tag"
RHGYLWAAALVRRWLEQEELPGATLVIATSGAVTVSDDDSVPEPGAAAMWGVIRCAQA
ESPDRFYLLDTDAEPGMLPAVPDNPQLALRGDDVFVPRLSPLAPSALTLPAGTQRLVP
                                                                                                EGELHALDWVRLAEPGSTGRVVAADASDLDAVLRSGEPEPDAVLVRYEPEGDDPRAAA
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DLGEAGVDELLEALGRELDGDGNSHHHHHH"
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/db_xref="GI:54778586"
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/product="BryAII (morphed)"
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10947. .21677
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10933. .10938
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RESULT 10 AB088224/c

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DEFINITION

AB088224 210614 bp DNA linear BCT 11-Streptomyces rochei plasmid pSLA2-L DNA, complete sequence AB088224

BCT 11-JUN-2003

ACCESSION POCUS

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Matches 359;
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                                                                                                                                      CTGATGCGCTGAGCACCGTAGTATCGCTGTTAAGCCGTG----ATGGCGAGGCTGTCG 24868
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GCG 25051
                                                  GIG 600
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                                                                                                                                                                                                                                                      CCCTGTGGCTGGTGACCAGGGACGCCGCCGCCGTGACCGTCGAGACGACGTCGATCCGG 537
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                                                                                                   CCCAAGCCATGGTGGGCGGGCTGGGCCGTCGTTGGTATCGAACAACCGGGTCGCTGGG 25048
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21829. .21853
/note="lac operator"
21860. .31407
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LRDAGDFRGRYAFPDLGEAGDDRLGEILREVYGLLGAGELDRLYSSAMELGSAPAALQ
LRDAGDFRGRYAFPDLGEACDDRLGEILREVYGLLGAGELDRLYTENGSWELLGLVERRG
LMSRGRHVGKLVLTQAFPVDPDGTVLITGGTGTLGALFRLVTENGVTHAAGVLADGL
ADAFGSDELAAEIEDLGASAEIAACDTADRDALSALLDGLFRFLTGVVHAAGVLADGL
VTSIDEFAVEQVLRAKVDAAMNLHELTANTGLSFFVLFSSAASVLAGFGQGVYAAANE
SLNALAALRTRGLFAKALGWGLWAQASEMTSGLGDRIARTGVAALFTERALALFDSA
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SDQVAGLAELVRSHAAAVSGYGSADQLPERKAFKDLGFDSLAAVELRNRLGTATGVRL
PSTLVFDHPTPLAVAEHLRDRLSSASPAVDIGDRLDELEKALEALSAEDGHDDVGQRL
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Pred. No. 1.6e-09;
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Submitted (15-JUL-2002) Haruyasu Kinashi, Hiroshima University,

Department of Molecular Biotechnology, Graduate School of Advanced

Sciences of Matter; 1-3-1 Kagamiyama, Higashi-Hiroshima, Hiroshima

739-8530, Japan (E-mail:kinashi@hiroshima-u.ac.jp,

Tel:81-824-24-7869, Fax:81-824-24-7869,

Tel:81-824-24-7869, Fax:81-824-24-7869

The nucleotide sequence has been determined by using restriction

fragments and nested deletion fragments of the ordered cosmid

library of pSLA2-L.

pSLA2-L is 210,614 bp long with G+C content of 72.8 % and carries

143 ORFs.
                                                                                                                                                                                                                                                                                                                                                            http://www.nih.go.jp/~jun/cgi-bin/frameplot.pl. Where possible we chose an initiation codon (atg, gtg, ctg or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13 bp before the initiation codon). If this could not be identified we chose the most upstream initiation codon.

Three-fourths of the pSLA2-L DNA are occupied by biosynthetic genes (three PKS gene clusters for lankacidin, lankamycin and an unknown type II polyketide, a carotenoid biosynthetic gene cluster, many regulatory genes and others). The range of each biosynthetic gene cluster has been deduced by comparison with similar gene clusters in most cases and may be revised in future.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mochizuki,S., Hiratsu,K., Suwa,M., Ishii,T., Sugino,F., Yamada, and Kinashi,H.

The large linear plasmid pSLA2-L of Streptomyces rochei has an unusually condensed gene organization for secondary metabolism Mol. Microbiol. 48 (6), 1501-1510 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene prediction was based on the unique codon usage in Streptomyces (Bibb et al., Gene 30:157-66 (1984)) using the FramePlot program of Ishikawa and Hotta (FEMS Microbiol Lett 174: 251-253 (1999)) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hiratsu, K., Mochizuki, S. and Kinashi, H.
Cloning and analysis of the replication origin and the telomeres
the large linear plasmid pSLA2-L in Streptomyces rochei
Mol. Gen. Genet. 263 (6), 1015-1021 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification of two polyketide synthase gene clusters on the linear plasmid pSLA2-L in Streptomyces rochei Gene 246 (1-2), 123-131 (2000)
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Physical mapping of the linu
the eryAI and actI homologs
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                                                 /note="left terminal inverted repeat, TIR-L; shows 99.4 $
(1981/1992) sequence identity to TIR-R (complement
(208623...210614))"
                                                                                                                                                                                               /db_xref="taxon:1928"
/plasmid="pSLA2-L"
                                                                                                                                                                                                                                                                                                                                              1. .210614
/note="N-terminal sequence is almost identical (435/437)
                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="7434AN4"
                                                                                                                                                                  'note="linear plasmid"
                                                                                                                                                                                                                                                                                                              organism="Streptomyces
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he_linear plasmid pSLA2-L and localization of
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/db_xref="G1:30698346"
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/translation="MSTTSRTDOREAAQQEAVDAVVRALELPVRLLAPERGLRTQVIM
/translation="MSTTSRTDOREAAQQEAVDAVVRALELPVRLLAPERGLRTQVIM
/translation="MSTTSRTDOREAAQTEAVDAVCALERAHRGGLPGMDLIVVDEAHRT
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SGRLGKPMAVVHDNTR1PSLRRLYMTATPRLMGLDEDABCAPGELVASMEDDPGGLPG
ARCFTLITLSEAIDRGICAPYQVVCVDITDTQLQAAQLLGVEGRSDEVRGARLAALQTA
LLKASSEENFRRTLVFHHMYKEARAFAAGLPUVARKRLHAAGPGLYPRTIMAMMLCGEH
KPGHRARVLGEFTSGLATUGTVVTEKGETLSVKYLGEGVDTTRECDSVYMADVRGSMPDL
VQAVGRALRIQPGQGKVASLVVPVLLDPGETADNMLTSRPYNGLALLFRQAPLLTGHG
EEGFFAAARFPGFEVRPVLGVRGAGASAGPASRSITPSAMSSLSISMRAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with that of (inner end of CORF1 (501 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
/product="putative secreted protein"
/protein id="BAC76460.1"
/db_xref="GI:30698347"
/translation="MRRKPRALLGIPLGLLVAVLAPAPAAHASADTYVGTWAAPPTAA
/translation="MRRKPRALLGIPLGLLVAVLAPAPAAHASADTYVGTWAAPPTAA
/translation="MRRKPRALLGIPLGLLVAVLAPAPAAHASADTYVGTWAAPPTAA
/translation="MRRKPRALLGIPLGLLVAVLAPAPAAHASADTYVGTAAPAAPPTAA
/phostvyfedgtlapctyllsvalpctyratswijplsgvsvdrragtadssvvtlcdbsirdgeht
yohnfvaagdvtgapdltpystatswijplsgvsvdrragtadssvvtlcdbsirdgeht
                                                                                                                                                                                                                                       /translation="millgtaagggfpqmncacalcargrrgblparggbcvavsgbg
rbmmlhaspblrgtagaltrgargl
TVyaappvrgallsablpvrgglldryapmbmpndpagafavlaggltvrahpvgryak
yahappppapmvcayribbparggalvyapclatmpdgfdbllasatcallbgtffsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4922. .5812)
/note="ORF4 (296 aa), lankacidin biosynthesis
similar to AE004625-4 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to Y00459-2 Streptomyces protein, StrR (350 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ORF3 (328 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TÜDADRRWEDLLABRIJRRDGGI.AGTGVVNAGIGGNRIJJRDPDEBFGSAARSFAAYFGB
SALKREDRDVIGGPGJRAVTVIJGVNDIGGPGI.ABPASDEVTARBLIAGYRQLIBRAH
BHGIJKIYGATITEFAGDIGYETERRBAVRQVNDWIRTSGAFDTVIJDFDAVIJRDPAR
PDHIJPAYDGGDGIJHPNDAGMAAMARAFFIJDSIJR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar to AE004736-10 Pseudonomas aeruginosa
protein (442 aa)"
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                                                          /note="ORF5 (364 aa),
similar to AJ277117-5
protein (359 aa)"
                                                                                                                                                 complement (5815. .
                                                                                                                                                                                   HAAVREAGVEVLPDGSELVL"
                                                                                                                                                                                                              GELGTATSSAGAGQSLMGHLPVAGPGGSLAALARHRGLRRIYTHLNNTNPLLDPSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyrroloquinoline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLLQCGAVERTALLAMAQTVPPHCTDLVABLAREYADLWABFAREVARTDG"
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                                                                                                                                                                                                                                                                                                                                                            /product="pyrroloquinoline
/protein_id="BAC76462.1"
/db_xref="GI:30698349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
/transl_table:
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/codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quinone biosynthesis
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                                                                                            Gluconobacter
                                                                                      ankacidin biosynthesis protein.
Huconobacter oxydans putative pqqE
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241 TACCCCCGGCCTGGACGGACGTCCGCGACGGCCTGGAACAGCGCGCGGGCGACCGT--
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                                                                                                                                                                 TCCCCTGGGCCGGGTCCCCGACACCACGACGAGTGGCGTTACCAGCTCGCCTGGCACC
                                           ACGCCGGGTGGGCGGCCGCCTCACCGGCCGCGTCCTGCTGGTGACCGGCCGCCGGC
                                                                                    CCGTCGACCTCGGGCGGTCCTCCCTGGCCGGACGGGTCCTGGTGACCGGAGCGGCAG
                                                                                                                               CCCCCGGCCGCCGCAACCCGCCGGCCGGGAACGGCGCTACCGGGTGCGGTGGCACG
                                                                                                                                                                                                                                                            AGGGACGCCGGTCGACCTGCCGGTCTACCCGTTCCAACGACAGAACTTCTGGCTCCCGG
                                                                                                                                                                                                                                                                                                       CGGCGCTCGGCGAGGCCCATGTGCGCGCGCGTCCAGGTCGACTGGAGCCCCGCGCTTTCGG
                                                                                                                                                                                                                                                                                                                                                CCGCGCTCGCCGAGGCGTACACCCCGGGGGGGGTGGAGGTCGACTGGCGTACCGCAGTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein similar to AL133424-19 Streptomyces coelicolor putative ABC transporter ATP-binding protein (544 aa) mark=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="pyrroloquinoline quinone biosynthesis protein C"
/protein_id="BAC76465.1"
/db_xref="Gl:3069832"
/translation="MSMSVTREVAAPWSEABFRORLHALESSYWDRHPFHRRWHEGLL
/begelemwyyorclpokoaatvancplpevrRowlsatvyhocadackgcaek
WIRLAEAVGEREDEVHDERLVLAGTRFAVDAYVDFARRFWHEAAASGITELFSPGIL
AHRLGREREHYPWIAEBGFEYFTARIEVVGPEGRSILDLVARHAVSREOCEACVRALA
FKCRVLNAVLDSLDYHTGNGATRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (7926. .8030)
/note="ORP8 (34 aa), lankacidin biosynthesis protein similar to AL603642-197 Sinorhizobium meliloti putative pyrroloquinoline quinone biosynthesis protein A (31 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="madpavgapagmlielthrcplhcpycsnplelvrreaeliceg
WTDILTQARELGVVQMHFSGGEPLARPDLPDLVGHARRLGAYVNLVTSGVGLTAERAH
DLARRGVDHVQLSLQDADPAAGQAIAGARVHTAKLEAARAVTAAGLPLIVNIVLHRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF7 (242 aa), lankacidin biosynthesis protein
similar to AE004625-5 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ORF6 (90 aa), lankacidin biosynthesis protein similar to AL603642-200 Sinorhizobium meliloti putative pyrrologuinoline quinone biosynthesis protein D (98 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDRTGRMVDLAVDLGADRIELANTQYYGWGLRNRAALMPTAAQLAAAREAVRHARTRY
AGGPELVYVAADYYDDRPKPCMDGWGSTQLTVTPAGDVLPCPAAYAITTLPVENALRR
PLSELWYASBSFNAYRGTGWMBEPCRTCPERHADHGGCRCQAFQLTGDAAATDPACGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="pyrroloquinoline quinone biosynthesis protein A"
/protein_id="BAC76466.1"
/db_xref="GI:30698353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyrroloquinoline quinone biosynthesis protein C (250 aa)"
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LAHCDGTTSLAGIVERLAEEYEGVSAEDVRELLLRLAQRRVVDLHG"
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/protein_id="BAC76464.1"
/db_xref="GI:30698351"
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/protein_id="BAC76463.1"
/db_xref="GI:30698350"
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56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                           Gape
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Location/Qualifiers
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/mol_type="unassigned DNA'
/db_xref="taxon:47853"
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Location/Qualifiers
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Micromonospora carbonacea
Bacteria, Actinobacteria, Actinobacteridae; Actinomycet
Micromonosporineae; Micromonosporaceae; Micromonospora.
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                              GAGCGGCAGTACCCCCCGGCCTGGACGGACGTGGTCCGCCACGGCCTGGAACAGCGCGGGG
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/mol_type="unassigned DNA"
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Biosynthesis of the polyene antifungal antibiotic nystatin in Streptomyces noursei ATCC 11455; analysis of the gene cluster deduction of the biosynthetic pathway Chem. Biol. 7 (6), 395-403 (2000)
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Streptomyces noursei ATCC 11455
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-MAY-2000) Unigen,
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                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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4714. .5748
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/note="polyketide synthase"
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Best Local Similarity
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                                                                                                                                                           Sequence 35
AX211739
AX211739.1
                                                                                   Streptomyces noursei
Streptomyces noursei
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Gene cluster encoding a nystatin polyketide manipulation and utility Patent: WO 0159126-A 35 16-AUG-2001;
                                                                                                                                 Streptomyces noursei
                                         Gulliksen, O.M.
                                                 Zotchev, S.B., Sekurova, O.N., Fjaervik, E., Stroem, A.R., Valla, S., Ellingsen, T.E., Sle
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    Brautaset, T.,
    Sletta, H.V. and

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RESULT 15
AX697991
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11238 bp Sequence 15 from Patent WO03010193. AX697991 AX697991.1 GI:29499041

DNA

linear

PAT 02-APR-2003

Micromonospora carbonacea Bacteria; Actinobacteria;

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Actinobacteridae; Actinomycetales;

t,C.M., Staffa,A. and Yang,X. and proteins for the biosynthesis

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REFERENCE AUTHORS TITLE

Genes Farnet, C.M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 03010193-A 15 06-FEB-2003;
Ecopia Biosciences Inc. (CA)
Location/Qualifiers
                                                                                                                                                   GGTGACCAGGGACGCCGCGCGCGTGACCGTCGGAGACGACGTCGATCCGGCCCAGGCCAT 547
                                                                                                                                                                                                                                                               COTGOTGGCGCTCGCCGAGGGCGCGACGCGCCACCGGCCGTACCGCTCGGCCTGAC 3248
                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCCGCGACGGCCTGGAACAGCGCGGGGGGGGGCGACTCGCGTCGTTGTTGTGCACCGCGCAGTCGCG 322
                                                              GTGTGGGGGCTCGGCCGGGCCCTCGAACTGCCGGACCGATGGGGCG 3421
                                                                                   GETCACCCGGGGGGCCGTCGCCGTGTCCTCCGGCGAGGTGCCGGACGCCGGGCAGGCCCA 3368
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: gb_ba:*
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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16 17 18	13 14 15	110 110 110 110	Result No.
207.6	220.2 220.2 210 210	397.8 397.8 397.8 397.8 397.8 378.4 378.4 278.2	Score
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161			BQ 1
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AB089954 Micromono CQ875927 Sequence AY899214 Streptomy	AX697993 Sequence AX697977 Sequence AB070940 Streptomy Continuation (37 o	AP263245 Micromono AX112026 Sequence M63677 S.erythraea AR049368 Sequence AR095529 Sequence AR09556 Saccharop X56107 S. erythraea X62569 S.erythraea AY771999 Synthetic AY623658 Aeromicro AB088224 Streptomy	Description

## ALIGNMENTS

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	CDS	gene	000	FEATURES	TITLE JOURNAL	REFERENCE	JOURNAL	AUTHORS TITLE	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 AF263245 LOCUS DEFINITION
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2072. .3382
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928. .2061
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RESULT 2
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Pred. No. 6.5e-52;
; Mismatches 0;
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Bacteria; Actinobacteridae;
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TDP-4-keto-6-deoxyglucose-2,3-dehydratase; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product; megDV, TDP-hexose
4-ketoreductase (eryBIV, dnmV homolog),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mrveelgiegvftftpQtfadergvfgtayqedvfvaalgrple
pvaqvsttrskrgvvrgvhfttmpgsmakyvycargramdfavdirpgsptfgraepv
elsaesmvglylpvgmghlfvsleddttlvylmsagyvpdkeravhpldpelalpipa
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6592. 7197
/note="unnamed protein product; megDIV,
TDP-4-keto-6-deoxyglucose 3,5-epimerase;
homolog), TDP-4-keto-6-deoxyhexose 3,5-epimerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transI_table=11
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/translation=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLDLVMSERDRVAPTLREARDQGILPDYAACRAAAHRVVRT"
7220. .8206
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/transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product; megBII-1(megDVII),
TDP-4-keto-L-6-deoxy-hexose 2,3-reductase; SEQ ID NO: 10=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (8228. .9220)
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transferase, mycarose glycosyltransferase; SBQ I
translated amino acid sequence"
                                                                                                                                        complement (9226. .10479)
                                                                                                                                                                                 WVLSRPGILGAVIGPRTPEQLDSALRAAELTLGEEELRELEAIFPAPAVDGPVP"
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/transl_table=
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/transI_table=
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                                                           CGGGAGCGGTTCGTCGAACTGTTCACCGCCGCCCGCCGCCGGCCCCTCTTCGACGAACTC
                                                                                                                 GAGGAGCTGCGGACCACCCTGGACGCCGGGGACCCGTGGGTGTCGGTGGTGGACCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGCGGCGACTACCTGCGCAGCCAGGGCCTGCGCGCCATGGACCCGCAGCGGCGATC
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gg

Sg

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100.0%;

Score 601; DB 6; Pred. No. 6.5e-52; ; Mismatches 0;

Length 47981; Indels

0

Gaps

0

37805 300

240 37685 180 37625 120 37565 60

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(Translation-multuped)
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LPAIYGHSGPSGQTGRGVVTAMIRRALAGEPITMWHEGSVRRNLLHVEDVATAFTAAL
HNHEALVGDVWTPSADEARPLGEIFETVAASVARQTGNPAVPVVSVPPPENABANDFR
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glesyhtrtilfyngssvvpgwlttsdovrvvcftggysalgi svpqrftlatlar 
fdgeivttrsgldpasvpdnvrlvdfvpmnillpgcaavihhggagswatalhhgvpq 
isvahewdcylrgqrtaelgagvflrddfvdadtlwqalatvvedrshaenaeklrqe
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4-keotreductase, TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SEQ ID NO: 12= translated amino acid sequence"
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translated amino acid sequence"
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TITLE
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S.erythraea second and third ORF's of eryA gene, complete cds.
M63677
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Donadio,S., Staver,M.J., McAlpine,J.B.,
Modular organization of genes required
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Saccharopolyspora erythraea
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DTAAAEDVEGYSVTGVAPAVASGRISYTMGLEGPSISVDTACSSSLVALHLAVESLRK
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LSEARRRGHEVLAVVRGSALNQDGASNGLSAPSGPAQRRVIRQALESCGLEPGDVDAV
EAHGTGTALGDPIEANALLDTYGRDRDADRPLWLGSVKSNIHTQAAAGVTGLLKVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source text: Saccharopolyspora erythraea DNA
ALRNGELPATIHVEEPTPHVDWSSGGVALLAGNQPWRRGERTRRARVSAFGISGTNAH
VIVEEAPEREHRETTAHDGRPVPLVVSARTTAALRAQAAQIAELLERPDADLAGVGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="eryA ORF2 encoding modules 3 & 4 for
6-deoxyerythronolide B formation6-deoxyerythronolide
formation; putative"
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19. .10722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Saccharopolyspora erythraea"
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LSGEGGMAAVALGBAAVRERLE MOODRLS VAAVNGERS VAVSGEBGALRAFSEDCAAE
GIRVED IDVDYASHS POIERWREELETTGO IA REPARVTEHS TYERSK MOCTELDAR
YWYRKLERTVERDANYTELABS CYDE TE TEVSE PHYVOAV KERSK MOCTELDAR
YWYRKLERTVERDANYTELABS CYDE TE TEVSE PHYVOAV KERSK MOCTELDAR
YWYRKLERTVERDANYTELABS CYDE TE TEVSE PHYVOAV KERSK VERDGAEDA VVVGS
LHROGGDLS AFLRSMAT TAH VSGVDI IRNDYAL PGAAPEA VERCHANAGAEDA VVVGS
LHROGGDLS AFLRSMAT TAH VSGVDI IRNDYAL PGAAPEA VARCHANAGAELA KERSK VERDGAEDA VVVGS
LHROGGDLS AFLRSMAT TAH VSGVDI IRNDYAL PGAAPEA VARCHANGAELA KERSK VERDGAEDA VVAGS
LYKRILARS VERDE TE KRESGRILDDWILVTFLI IS PERTIEM CEARLE VERDGAEDA VVAG
LVKRILARS VERDE TE KRESGRILDDWILVTFLI IS PERTIEM CEARLE VERDGAEDA VAR
HAGTLITMES IS EX AR BEERAT IA KRYALLA VLDSUAGAEN VERCHANGAEDA VAR
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HAGTLITMES IS SEX VERSE PAT TA KRYALLA VLDSUAGAEN VERCHANGAEN VERCHANGAEN

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4171. .4428 module 3'" 1693. 3406. /note="putative"
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function="'approximate span 3406. .3921 /gene="eryA" /note="putative"
/function="'approximate
of module 3'" note="putative"
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                                                                               ARREGRE PULAULREGA WOOGASMOLTIN-REGRAQOR VI REALEMANDE OLIMINATION ARREGRE PULAULREGA WOOGASMOLTIN-REGRAQOR VI REALEMAGVIRAGUNYVEAH
GTGTRIADP I EVHALLSTYGARRDPDDP IMIGSYKSNIGTYGAAGVIRAGVINYVEAH
GTGTRIADD I EVHALLSTYGARRDPDDP IMIGSYKSNIGTYGAAGVIRAGVINYVEAH
HGEMPRTLHPDEPS PQI EWDLGAVS VVOGARS WPAGRER PRAGVER SEGISGTNAHVI V
ERAPEADDS PEPARDS GGPVPLU-USGRDEGAMRAQAGRILADHLARER PRISILDTGTTATI
RESAWEHRAVVUGDRDDALAGILRA VADGRI ADRTATGQARTRRGVANVPPGQGAQWQG
MARDLLRESQ VPADS I ROCERALA PHVUWSLITDLLSGARFDERVDVVQPALP AVMVSL
AALWRSHGVEPARAVVGHSQGSI LAAHVAGALTILEDAKULAVESR VLARLGGGGGAGAS
FGLGTEQAAERIGR FAGALS I AS VNGPRS VVVAGESGPLDELI AECEAEGITARRI PV
DYASHS PQVESLERELLTSLAGI SPVSADVALTSTTTGQPI DTATMTTAY WYXALIREQ
VREQDATRQLAREGEDA PVESSEPHPULTYGI BAYLDSALDAGACVUGTLERDRGGL
ADPHTALGEAY AQGVEVDWS PAFADAR PVELP VY PPQRQR YMLP I PTGGRARDEDDDW
RYQVVWRRAEWESSASLAGR VLLVTG PGGVESSEDS I RSGLAAGVALP LI PTGGRARDEDDDW
RYQVVWRRAEWESSASLAGR VLLVTG PGGVESSEDS I RSGLAAGVAF PLAVLTCD VESRSTI
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RYQVVWRRAEWESSASLAGR VLLVTG PGGVESSEDS I RSGLAAGVAGATULT COVESRSTI
RYQVVWRRAEWESSASLAGR VLLVTG PGGVESSEDS I RSSLAAVLAD PRGEEQV
ALIRADDIA VARLY VAR PARDARTWS PRGTVVLVTGGTGGIGAHVOR WILLAGSGAEHLVLL
GRIGAAD PAGASIR EEGLTALGTGVT I AVCUVADRAGAGT VLRAGAGGREPLWVLTRIAVQV
ALIRADGII VARLY VAR PARDARTWS PRGTVVLLDELC PDELDAFVLE SSNAGVWGS PGLASY
AAANAFLOGFARRRS GAAVTSGATATA KHRE PEDES I AGARAERGGSEERPLAQR
LAALSTAERELTALGT I TYRLADHYLGHGANAGDRGCAT VLRAGVERGS PGLAGA
VTGVREAATVEDHFT I TYRLADHYLGHGADAGABCAGALLT REFERDAGGEFERPLAGR
LAALSTAERET LAHLD PQQRQVLSTTWSLFENAGID PHSILRGSDTGVFLGAAY
VTGVREAATVED HYGT SKRAGABAVAGVAGVAVVLGLIGGAAP VTGTAGSSSLVALHSAC
GGSLRDGDGGLA VAGGUS WAT WAT VARAGARGVARAGVAGVAV
VLLQRLSOARRAGROVLGVVAGSA VAVOGRCKAR SEADAGFFREAGVAV
VLLQRLSOARRAGROVLGGVVAGSA VAVOGRCKAR SEADAGFFRAGGVAGVAGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGARGVAGAR
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of module 4'"
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FGISPREALAMDPQQRIMLEISWEALERAGHDPVSLRGSATGVFTGVGTVDYGPRPDE
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IKVVLGLNRGLVPPMLCRGERSPLIEMSSGGVELAEAVSPMPPAADGVRRAGVSAFGV
SGTNAHVIIABPPEPEPLPEPGPVGVLAAANSVPVLLSARTETALAAQARLLESAVDD
SVPLTALASALATGRAHLPRRAALLAGDHEQLRGQLRAVAEGVAAPGATTGTASAGGV
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GLALAGGVTVMSSPGÄFTEFRSQGGLÄÄDGRCKPFSKÄÄDGFGLÄEGÄGVLVLQRLSÄ
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/db_xref=
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/note="putative"
/function="'approximate
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/note="putative"
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/function="'appr
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6-deoxyerythronolide B formation; putative"
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/note="putative"
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VDVVQPVLFSYMVSLARLMGACGVSPSAVIGHSGGEIAAAVVAGVLSLEDGVRVVALR
AKALRALAGKGGMVSLAAPGERARALIA PMEDRISVAAVUSPSSVVVSGDPBALAELV
ARCEDBGVRAKTLFVDYASHSRHVEEIRETILADLDGISARRAAIPLYSTLHGERRDG
ADMGPRYMYDNLRSQVRFDEAVSAAVADGHATFVEMSPHPVLTAAVQEIAADAVAIGS
                                                   LHRDTAEEHLIAELARAHVHGVAVDWRNVFPAAPPVALPNYPFEPQRYWLAPEVSDQL
ADSRYRVDWRPLATTPVDLEGGFLVHGSAPESLTSAVEKAGGRVVPVASADREASAAL
REVPGEVAGVLSVHTGAATHLALHQSLGEAGVRAPLWLVTSRAVALGESEPVDPEQAM
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DB 1;

Length

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Sequence 3 :
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1 (bases 1 to 20235)
Katz,L., Donadio,S. and McAlpine,J.B.
Recombinant DNA method for producing
Patent: US 5824513-A 3 20-OCT-1998;
Location/Qualifiers
                                                                              Unknown.
                                                                                           Unknown
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                                                                  Unclassified
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Pred. No. 1.5e-31;
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Best Local Sim:
Matches 474;
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Sequence 3
AR095529
AR095529.1
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                                     1 (bases 1 to 20235)

Katz,L.; Donadio,S. and McAlpine,J.B.

Method of directing biosynthesis of spatent: US 6004787-A 3 21-DEC-1999;

Location/Qualifiers
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                                                                                                 Unclassified.
                                                                                                          Unknown
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         /organism="unknown"
/mol_type="unassigned
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78.9%;
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Pred. No. 1.5e-31;
0; Mismatches 127;
                                                                                                                                                                20235 bp
US 6004787.
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                                       Total synthesis of long DNA sequences: Synthesis 32-kb polyketide synthase gene cluster Proc. Natl. Acad. Sci. U.S.A. 101 (44), 15573-155 2 (bases 1 to 32299)
Hu,Z. and Reid,R.
                                                                                                                        Saccharopolyspora erythraea
Saccharopolyspora erythraea
Bacteria; Actinobacteria; Actinomycetales;
Beudonocardineae; Pseudonocardiaceae; Saccharopolyspora.
1 (bases 1 to 32299)
Kodumal, S.J., Patel, K.G., Reid, R., Menzella, H.G., Welch, M. au
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Saccharopolyspora erythraea promplete sequence.
AY661566
AY661566 GI:55419414
Direct Submission
Submitted (21-JUN-2004)
Hayward, CA 94545, USA
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FEATURES

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ANUTRELIVADYWRRS PILLPWREDEA IRSALEWGREIT YEASE PHYLARALAGOTLIARG
SSANVETLOGGGGGRER FILLAANACHTGOTKU WUTTAN YEUNGASERGEI PERE PABLESS
EPPAB SGUDMIA PHYLLERILLA VUNGETAALAGREADARAT FRELGILDS VLAAQIRA
KVSBA IGREVAI ALLYHHFT PRALAEALAAGTEVAA GRETRARTIRESGEN PERE PABLESS
DEPAB SGUDMIA PHYLLERILLA VUNGETAALAGREADARAT FRELGILDS VLAAQIRA
KVSBA IGREVAI ALLYHHFT PRALAEALAAGTEVAGRETRARTIRESGTAHGRGGFUTAVAWA
CRLHGGYST PERE PHELLESGEDAN VAGLETDRAWDLDSL'HHDDTRSGTAHGRGGFUT
EATA FDDA FORMS PERLAVDDPQREMIELSAWFULDSL'HDDTRSGTAHGRGGFUT
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KONLLARIS GREVALATULA VLRGTAVASGA IS LLDER PERPAGARLAGTAGAGA
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GRUDVYQVPARA VWYSLASHISHIET I DALHEELGEDDHE DE GWPE FEST VURKGRUDAR
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ALHSIGKAGA VULLET SE PAAA FA PAGEVRAA I GDR VEI FA ANVREP SE VYAGALS LIDARKVA
CTURES VERTUR SELGGTE HAT VIRAGGES PHILLI VERROGGEN LORAKVA DE TOTA BREADARAT ANACH
LEYVAKAS ELIGGTE MYTTE SE PAAA FACHGAS DAALAS LAGART TVAACD
VUDRAS VERTUR SELGGTE HAT VARACH PHILLI VERROG DLAAGAGE LAARSAACHACH
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LEGRAL VUDRA SELGGE BAD VULLE REGURD FOLLE REGURD FOLLE REGURD FOLLE HAT VARACH PHILLI VERROG PLAAGAGE LAARDAACHACH
VUDRAS VERTUR SE PAAAGARACH FERRAL TO SARAVLAD TA ANACH
VUDRAS VERTUR SE PAAAGACHACH SEREAL FELVER HAT ANACH
LEGRAL VUDRA SELGGE BAD VULLE ARROCALD BAD VERTUR SELGCA VERSALLAT TORAGRA VUDRA
REGURDA VURGA BAD ANACH SELGCA TO SARAVLAD TA SARAV
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AALWSSEMIPLVGNGNGAAVALSADEIEPRIAWDDDVVLAGVNGPRSVLLTGSPEPV
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PVRELVHGLIEQGDVVRGVVHAAGLPQQVAINDMDEAAFDEVVAAKAGGAVHLDELCS
                                                TAGLGAEVARWLAGRGAEHLALVSRRGPDTEGVGDLTAELTRLGARVSVHACDVSSRE
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PHMPDPELRGRLTAVLAGSEDQVAVRADAVRARRLSPAHVTATSEYAVPGGTILVTGG
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LLDRI VTTAPSERAGEÞETESLRDRLAGLPRAERTAELVRLVRTSTATVLGHDDPKAV RATTPFKELGFDSLAAVRLRNLLNAATGLRLPSTLVFDHPNASAVAGFLDAELGTEVR GEAPSALAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGD DLGEAGVDELLEALGRELDGD"

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gene SdO

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GESSMAVVGGAAVMATPGVFVDFSRQRALAADGRSKAFGAGADGFGFSEGVTIVTLERK lrrggevvfplsinrsalrraefvpevlrgmvraklraagqabaagpnvvdrlagrsb

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Query Match
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RYQVVWREABWESASLAGRVLLVTGPGYPSELSDAIRSGLEGGATVLTCDVESRSTI
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ESLLRRWNSRRADAPSTSAISEDASDDELFSWLDQRFGGGEDL"
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/db_xref="GI:55419417"
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Saccharopolyspora erythraea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Location/Qualifiers
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/db_xce="005.00133"
/db_xce="005.00133"
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FGISPERALAMDP,QRIMLEISMEALERAGHDPVSLERGSATGVFTGVGTVDYGGPRDE
APDEVLGYVGTGTASSVASGRVAYCLGLEGPAMTVDTACSSGLTALHLAMESLERDEC
GLALAGGVTVMSSPGAFTEFRSQGGLAADGRCKPFSKAADGFGLAEGAGVLVLQRLSA
ARREGREVLAVLAGSANNODGASNGLTAFSGGAQGNVIRRALENAGGVRAGDLYVDELSA
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PAAAPWEGVVVGGARDALSAGLRAVADERRIADTSLSGARLADHLAASRGTRCATFVSGAWQGM
ARDLLESGVVPADSIEDCERALAFHDWSLTDLLSGARPLDRVDVVDPALFAVWFSLA
ALWRSHGVERDALSINGLASVNGFRSVVVVAGESGFLDELIAGGCQGAMSF
GLGTEGAARTAGALSIASVNGFRSVVVVAGESGFLDELIAGGCRAMSF
GLGTEGAARTAGAALSIASVNGFRSVVVVAGESGFLDELIAGCERABAKKARRIFV
DYASHSPQVESLREELLTELAGISPVSADVALYSTTTGQFIDTATMDTAYWANLREG
GLGTEGAARTAGAASILASVNGFRSVVVVAGESGFLDELIAGCERABAKKARRIFP
DYASHSPQVESLREELLTELAGISPVSADVALYSTTTGQFIDTATMDTAYWANLREG
GRANDEDDDWRYQLAERAGALSIASVNGFRSVVLVVGGSGATVLT
CDVSRSTIGTALEAADTDALSTVGYAAVPHGEGAVDPSELSDAIRSGLAGAGVWAFUL
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ADPRGEEQVAIRADGIKVARLVPAPARARTHPLEPLAGTVLTGGIGAHLARWLARSG
RAELIVLLGARGASELEREETTAJGTGTTAACOVADARALERAVLAAAEAAAAEGRT
VGANWAM AGUGGTGTDI,INITEREFTETATGTTAACOVADARALERAVLAAAEAAAAEGRT
VGANWAM AGUGGTGTDI,INITEREFTETATGTTAACOVADARALERAVLAAAEAAAAGRT
VGANWAM AGUGGTGTDI,INITEREFTETATGTTAACOVADARATARANGAWAAAAAGRT
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57 occ
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/transT_table=11
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/mol_type="genomic DNA"
/strain="NRRL 2338 (sub-species)."
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Query Match Best Local Similarity mat\_peptide 4038 3978 3918 4218 4158 4098 3858 418 361 301 241 181 121 470; 61 ш GAGGGCGGCCACTACCTGCGCAGCCAGGGCCTGCGCGCCATGGACCCGCAGCGGGCGATC GGGCTGCCGGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGGCAGAACATGGCCGGTACC GCCTCCTACGCGGCGAGCAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT GAGGAGCTGCGGACCACCCTGGACGCCGGGGGACCCCGTGGGTGTCGGTGGGACCTGGAC 240 GAGGGCGGCGAGTACCTGCGCAGCCAGGGCCTGCGGGCCATGGACCCCGGATCGGGCCGTC GGCGCGCCGGTGACGTCCATCGCCTGGGGGCTCTGGGCCGGGCAGAACATGGCCGGGGAC GTGGCAGCGGTGCTGGGCCACGGCACGCCGACGGTGATCGAGCGTGACGTCGCCTTCCGT CGGGAGCGGTTCGTCGAACTGTTCACCGCCGCCGCCGCCGGCCCCTCTTCGACGAACTC GCGGCGCTGTGCGACGGCCGAGAGCGCGAGCACCTCGCCCACCTGATCCGCGCGAG фенератизет в предоставание по предоставление по предоставлени GCCGGTGCCCGGGAAGCCCGGCAGAGCGAGGAGGGCCCCGGCGCTCGCCCAGCGGCTC GGTGGGGTCCGCGGGGGGGGGGGGGGGGGGGGCTCAGGAATCGGATCTCGCCCGGCGGCTG SSIVALIBACGES DEDGCLAVAGOVS WAAGPEWFTEFERQGILAVDGRCKAFSAEAD
GFGLPECVAVVQLQRLSDGPDEGLAVAGGVSWAAGPEWFTEFERQGGLAVDGRCKAFSAEAD
GFGLPECVAVVQLQRLSDGPDAEGGRQVLGVVAGSAINQDGRCKAFSAEAD
GFGLPECVAVVQLQRLSDGPDAEGGRQVLGVVAGSAINQDGRCKAFSAEAD
KAMARAGITGADVAVVEAHGTGTTRLGDPVCBASALLATYGKSGSSGPVLLGSVKSNIG
HAQAAAGVAGVIRVULGLANGILVEPMLCRGERSFLIEWSSGGVBLAEAVSPPPLADA
VRRAGVGAFGVSGTNAHVII AEPPEPEPEPPLPEPEPCYGVLAAANSVPVLLSARTETALAA
QARLLESAVDDS VPLTALASALLATGRAHLPRAALLAGDHEQLRGQLRAVAEGVAAP
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ADAVAIGSLHRDTASEHLIAELARAHVHGVAUNGRUNFPAAPPVALPRVFFEPORYWL
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GVDAPAAAELARALVALGFTTITACUVADRSQLSGTFVARHLARCGVEDLVLVSRR
GVDAPAAAELARALVALGFTTITACUVADRSQLSGTLFALEGGHVARHLARCGVEDLVLVSRR
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VLIUVSPCHQODANAMILSELTATIORSTVANGGALMAYALATELLDRGRPGRFGL Conservative MDPDRAVEELHITLDHQQTSVSVVDMDRRRFVELFTAARHRPLFDEIAGARAEARQSE
EGPALAQRLAALLCDGREREHLAHLIEABVAAVLGHGDDAAIDRDRAFRDLGFDSMTA
VDLRNLAAVTGVREAATVVPHFTITRLADHYLERLABAEARDAPALVREVPFDRA
DDFIAIVGMACRFPGGVHUPGELWEFIVGGGDAVTEMPTDRGWDLDALFDPDPQRHGT
SYSRHGAFLDGAADFDAAFFGISFREALAMDPQGRQVLETTWELFENAGIDPHSVRGS
DTGVFIGAAYQGYGQDAVVPEDSEGYLLTGNSSAVVSGRVAYYLGLEGPAVTTDTACS /gene="eryA" /product="6-deoxyerythronolide B .9590 63.0**%**; 77.8**%**; 0 Score 378.4; DB 1; Pred. No. 1.6e-29; Mismatches 131; synthase" Indels Length 9769; ω --Gaps 120 3917 4037 3977 60 300 4097 180 4277 4217 360 4157 477 417

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GTCGCCGCGTGCTCGGCCACGGCGACGACGCGGCGATCGACCGCGACCGCCTTCCGC

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Saccharopolyspora erythraea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6-deoxyerythronolide B synthase; acyl carrier protein; acyltransferase; beta-ketoacyl synthase; dehydratase; enoyl reductase; ketoreductase; multifunctional subunits; thicesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEERYABS
S.erythraea erya
X62569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-SEP-1991)
Cambridge, Tennis Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-deoxyerythronolide B 1
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bridge, Tennis Court Rd, Cambridge CB2 1QW, UK
related sequences see X56107 & M63677.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ="SE55, DE10, pBK25"
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Query Match Best Local Similarity

63.0%;

Score 378.4; DB 1; Pred. No. 1.3e-29;

Length 20444

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db_xref="UniProt/Swiss-Prot:Q03133"
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/protein_id="CAA4449.1"
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/note="ORF A"
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Submitted (05-OCT-2004) Kosan Biosciences, 3832 Bay Center Place
Hayward, CA 94545, USA
Location/Qualifiers
                                                                                                                                                                                                    other sequences; artificial sequences.
1 (bases 1 to 31531)
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d,R.C., Kodumal,S.J.,
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                                                                                                                          Natl. Acad. Sci. U.S.A. 101 (44), 15573-15578
                                                                                                                                         synthesis of long DNA sequences: Synthesis of a contiguous polyketide synthase gene cluster
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                                              Submission
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misc_feature
                                                                                        //producein_id="styAi("morphed)"
//producein_id="styAi("morphed)"
//producein_id="styAi("morphed)"
//b xeef="q01:5479585"
//b xeef="q01:5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to Saccharopolyspora erythraea EryAI
GenBank Accession Number AY661566; contains His-tag
SEVAGFSVSEYLEPRÞDAPSLERVDVVQÞŸLFÄVMVSLARLMRACGAVÞSAVIGHSQG
EIAAAVVAGALSLEDGMRVVARRSRAVRAVAGRGSMLSVRGGRSDVEKLLADDSWTGR
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72. .77
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                                                                     LRAVADGAVVPGVVTGSASDGGSVFVFPGQGAQWEGMARELLPVPVFAESIAECDAVL
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/db_xref="taxon:32630"
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<u>Levaavngpdavvvagdaqaarefleycegvgiraraipvdyashtahvepvrdelvg</u>

ALAGITPRRAEVPFFSTLTGDFLDGTELDAGYWYRNLRHPVEFHSAVQALTDQGYATF
IEVSHPVLASSVQETLDDAKSDAAVLGTLERDAGDADRFLTALADAHTRGVAVOWEA
VLGRAGLVDLFGYPFQGKRFWLQPDRTTPRDELDGWFFWYDWTEVPRSBPAALAGRWL
VVVPECHEBDGWTVEVRSALAEAGAEBEVTTRGVGGLVGDCAGVVSLLALEGDGAVQTL
VLVRELDAEGIDAPLWTVTFGAVDAGSPVARFDQAKLWGLGQVASLERGFRWTGLVDL
PHMPDPELRGRLTAVLAGSEDQVAVRADAVRARRLSPAHVTATSEYAVPGGTILVTGG LLDRIVTTAPSERAGEPETESLRDRLAGLPRAERTAELVRLVRTSTATVLGHDDPKAV RATTPFKELGFDSLAAVRLRNLLNAATGLRLPSTLVFDHPNASAVAGFLDAELSSEVR GEAPSALAGLDALEAALPEVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGD TAGLGABVARWILAGRGABHLALVSRRGPDTEGVGDLTABLTRIGARVSVHACDVSSRE
PVRELVHGLI EQGDVVRGVVHAAGLPQOVAI NUMDBAADDEVVAAGGAVHLDBIJCS
DAELFILPSGAGVWGSARQGAVAGAUAFILDAFBARHRRGRILFATSVJAGGLVHACGGU
GDBEAVSFILRERGVRAMPVPRALAALDRVLASGETAVVVTDVDWPAFAESYTAARPRP DLGEAGVDELLEALGRELDGDGNSHHHHHH "

misc\_feature terminator 'note="lac operator" note="T7 terminator" .10861 .10899 promoter"

/gene="eryAII (morphed)" /note="similar to Saccharopolyspora erythraea EryAII of GenBank Accession Number AY661566; contains His-tag" /gene="eryAII (morphed)" 10947. .21677 /product="BryAII (morphed)"
/protein\_id="AAV39551.1"
/db\_xref="GI:54778586" /codon\_start=1 /transl\_table= /gene="eryAII (morphed)" 10933. .10938 \_table=11

SdS RBS gene

VPAADVDVVEAHGTGTELGDP I BAGAL I ATYGQDRDRPLRLGSVKTNI GHTQAAAGAA GVI KVVLAMRHGMLPRSLHADELSPH I DMESGAVEVLREEVPWPAGERPRRAGVSSPG VSGTNAHV I VEEAPAEQEAARTERGPLPFVLSGRSEAVVAAQARALAEHLRDTPELGL MNGQSYMQLLAGEAERVDGYQGLGNSASVLSGRIAYTFGWEGPALTVDTACSSSLVGI HLAMQALRRGECSLALAGGVTVMSDPYTFVDFSTQRGLASDGRCKAFSARADGFALSE GVAALVLEPLSRARANGHQVLAVLRGSAVNQDGASNGLAAPNGPSQERVIRQALAASG /translation="MTDSEKVAEYLRRATLDLRAARQRIRELESDPIAIVSMACRLPGGVNTPQRLWELLREGGETLSGFPTDRGWDLARLHHPDPDNPGTSYVDKGGFLDDAAGF tdaawtlatgrar*f*dvraavl*g*ddragvcaeldalaegrpsadavapvtsa*p*rkpvlv

> AHYALHDLAGLRAGQSVLIHAAAGGVGMAAVALARRAGAEVLATAGPAKHGTLRALGL
> DDEHLASSRETGFARKERERTGGRGVDVVLNISLTGELLDESADLLABGGVFVENGKTD
> LRDAGDFRGFKVAPFDLGEAGDDRLGES LREWGLLGAGELDELPVSAMELGSAPALD
> LRDAGDFRGFKVAPFDLGEAGDDRLGES LREWGLLGAGELDELPVSAMELGSAPALD
> MSRGRHVGKL-VLTQPAPVDPDGTVLITGGTGTLGRLLARHL-VTEHGVRHLLLLVSRRG
> ADAFGSDELRAS IEDLGASAES IAACDTADRIDALSALLDGLPRE LTGVVHAAGVLADGL
> VTS IDEPAVEQVLRAKVDAAMNLHBLTANTGLSFFVLFSSAASVLAGPGQGVYAAANE
> SINALAALRFTGGLPAKALGWGLMAGASEMTSGLGDRIARTGVRALPTERALALFDSA
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Query Match Best Local Sim Matches 401; gene misc\_feature Similarity Conservative /note="lac operator" 21860..31407 /note="T7 promoter" 21829. .21853 /gene≃"eryAIII (morphed)" 46.8%; Score 281; DB 11; Pred. No. 5.3e-20; 0; Mismatches 200; Length 31531;

terminator

note="T7 terminator"

맑 문 S 片 Ś S 밁 25771 25651 GCGTCCTACGCCGCTGCGAACGCGTTTCTTGATGGTTTCGCACGCCGCCGCAGATCTGAA 25710 181 121 61 GAGGAGCTGCGGACCCTGGACGCCGGGGACCCGTGGGTGTCGGTGGTGGACCTGGAC 240 GAGGGCGGCGACTACCTGCGCAGCCAGGGCCTGCGCCCATGGACCCGCAGCGGGCGATC 180 GAAGGCGGTGAGTATCTGCGTÄGCCAGGGCCTGCGCGCAATGGACCCAGATCGTGCGGTG 25830 GGCGCACCCGTCACGAGTATCGCATGGGGGTTTGTGGGCCGGTCAGAACATGGCCGGTGAT 25770 GEGETECCEGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGCAGAACATGGCCGGTACC 120 GCCTCCTACGCGGCGGCAACGCCTTCCTCGACGCCTTCGCCCGTCGTCGTCGGCGCAGT 60

25831 GAAGAACTGCATATCACGCTGGATCACGGTCAGACCTCCGTCTCAGTGGTCGATATGGAC 25890

GCGTCGATGCCGGAGGCGAACGTCACGAGCATGTCGCCCGGCTGGTCCGAGCCGAGGTG 420 GCGGGTGCACGGGCGGAAGCTCGCCAGAGTGAAGAGGGGGCCTGCGCTGGCGCAGCGTCTG 26010

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541 GTCCGGGTGGCCACGACCATCGTCTTCGACCACCCGACAGTGGACCGCCTCACCGCGCAC 600 CTGGGGTTTGACTCCATGACTGCCGTTGACCTGCGCAACCGTCTCGCAGCCGTCACGGGG 26190

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MY623658
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Sequence update by submitter
On Feb 14, 2005 this sequence version replaced gi:53794556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicago, IL 60612, USA 3 (bases 1 to 61845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brikun, I.A., Reeves, A.R. and Weber, J.M. Direct Submission Submitted (11-MAY-2004) Fermalogic, Inc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Ind. M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-FEB-2005) Fermalogic, Inc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ind. Microbiol. Biotechnol. 31 (7), 335-344 (2004)
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ionibacterineae; Nocardioidaceae; Aeromicrobium.
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                                                                                                                                                                                                                                                                                               note="ORFL2; dehydrogenase/reductase fabG family"
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codon_start=1
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                                                               complement (6997.
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                                                                                                                                                                                                                                                                                                                                                                                  gene="eryCV"
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Query Match
Best Local Similarity
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TGCCGGTCACCTCGATCGCCTGGGGTCTGTGGGCCGGGCAGAACATGGCCGGTACCGAGG 124
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complement(11160. .12323)
                                                                                                                                                                                                                                                                                                      complement (11160. .12323)
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                                                                                                                                                                                                                                                                                                                                 VRIDDLQGSAG"
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                                                                                                                                                           Score 263; DB 1;
Pred. No. 2.6e-18;
                                                                                                                                          Mismatches
                                                                                                                                       195; Indels
                                                                                                                                                                                 Length 61845;
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                                     and Kinashi,H.

The large linear plasmid pSLA2-L of Streptomyces rochei has unusually condensed gene organization for secondary metaboli Mol. Microbiol. 48 (6), 1501-1510 (2003)
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Three-fourths of the pSLA2-L DNA are occupied by biosynthetic genes (three PKS gene clusters for lankacidin, lankamycin and an unknown type II polyketide, a carotenoid biosynthetic gene cluster, many regulatory genes and others). The range of each biosynthetic gene cluster has been deduced by comparison with similar gene clusters in most cases and may be revised in future.
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The nucleotide sequence has been determined by using restriction fragments and nested deletion fragments of the ordered cosmid
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pSLA2-L is 210,614 bp long with G+C content of 72.8 % and carries
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vappnttdvbeludwurppdkvtvpatyasiglgtlerahrgglpgmdlivvdbahrt
sgrlckpwavuhdnutripslrtlymtatprlwgldedabageblusabedddgleg
arcftltlsbaidrgicapyqvcvditdtqlqaqllgvbgrsdevrgarlaalqta
llkassbenfrrtluphhvkbabapaaglpdvakrlhaapgglyprtwamwi.cgeh
kpghrrvlgetstottvpvklabappakglydvakrlhaapgglyprtwadyrgsmpdl
vqavgbalriqpbqcgkvaslvvpvlldpbgstanmittsrpynglalltrqdprlltgh
bebffaarfopergrpvlgvgaqrgasagpasrsitpsamsslsismap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF1
/translation="mrrkprallgiplgllvavlapapaahasadtyvgtwaapptaa
paadstvyedQtlrQTvHLSVagdsLrvrftnepgtspltigevhaarpaaQgpatav
dpgtdrvvrfggrpsatlapgtQrwsdpvalpttaggdlvislylpQrtpgstvhsaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to AL590463 Streptomyces coelicolor putative helicase, SCP1.136 (879 aa); homology is seen untill inner end of TIR-L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="N-terminal sequence is almost with that of ORF143 at the right end inner end of TIR-L
                                                                                                                                                                                                                                                              similar to AE004736-10
protein (442 aa)*
                                                                                                                                                                                                                                                                                                                           /note="ORF2 (426 aa)
                                                                                           /product="putative secreted
/protein_id="BAC76460.1"
/db_xref="GI:30698347"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative helicase"
/protein_id="BAC76459.1"
/db_xref="GI:30698346"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="left terminal inverted repeat, TIR-L; shows 99.4 $
(1981/1992) sequence identity to TIR-R (complement
(208623. .210614))"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:1928"
plasmid="pSLA2-L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Streptomyces"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                             transi_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="linear plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="7434AN4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .210614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (501 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _table=11
                                                                                                                                                                                                                                                                                                Pseudonomas
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                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                            aeruginosa hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identical (435/437) of pSLA2-L until the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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LAHCDGTTSLANGE (21771, 7899)
complement (7171, 7899)
/note="ORF7 (242 aa), lankacidin biosynthesis |
finilar to AB004625-5 Pseudomonas aeruginosa
similar to AB004625-5 Pseudomonas aeruginosa
similar to AB004625-5 Pseudomonas aeruginosa

lankacidin biosynthesis protein

റ

(250 aa)\*

/translation="msmsvtrevaapmseasfrqrlhalessymdrhpfhrrmhegll degelrlwaanrwyyqrclpqxdaaivancplpevrrqmlsrivyhdgadacaggaek

/transI table=11
/product="pyrroloquinoline
/protein\_id="BAC76465.1"
/db\_xref="GI:30698352"

quinone biosynthesis protein C\*

/product="pyrroloquinoline quinone biosynthesis protein D"
/protein id="BAC76464.1"
/brotein id="BAC76464.1"
/db xref="Gi:3069851"
/translation="MTGLPEPTVPRLRPGVRLTRDPARGELALLPERVVVLNDTAAAV
LAHCDGTTSLAGIVERLAESYEGVSAEDVRELLLRLAQRRVVDLHG"

codon\_start=1/transl\_table=11

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YQHNEVAAGDVTGAPDLTEVSTATSWHFLSGVGVDRRAGTADSSVVTLGDSITDGEHT
TLDADRRWEDLLAERLRRDGGLAGTGVVNAGIGGNRIDEBGGSAASSFAAYFGE
SALKREDRDVLGQPGARAVTVLLGVNDLGQPGIAAPASDEVTASELIAGYRQLIERAH
EHGLKIYGATITEFAGDTIGYETERREAVRQQVNDWIRTSGAFDTVLDFDAVLRDPAR
PDHLLEAYDGGDGLHENDAGMAAMARAFFLDSLR"
complement (6902. .7174)
/note="ORF6 (90 aa), lankacidin biosynthesis protein
similar to AL603642-200 Sinorhizobium meliloti putative
pyrroloquinoline quinone biosynthesis protein D (98 aa)
                                                                                                                                        /trainilation="MADPAVGAPAGMLIELTHRCPLHCPYCSNPLELVRREABLICEQ
WTDILTQARELGVVQMHFSGGEPLARPDLPDLVGHARRLGAYVLVTSGVGLTAKRAH
DLARRGYDHVQLSLQDADPAAGQAIAGARVHTMAKLAHVTAAGLPLTVNIVLHRGN
IDRTGRMYDLAVDLGADIELAAQQAIAGARVHTMAKLAHVTAAGLPLTVNIVLHRGN
IDRTGRMYDLAVDLGADIELAAQTAGARVHTMAKLAHVTAAQLAAREAVRHARTRY
AGGPELVYVAADYYDDRPKPCMDGMGSTQLTVTPAGDVLPCPAAYAITTLPVENALRR
PLSEIWYASRSFNAYRGTGMMREPCRTCPBRHADHGGCRCQAFQLTGDAAATDPACGL
SPHRSLVDAALAEVTDGPVPAFVPRGFVPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTAALAGNLDQETRSIPISSLVPGYSPRLCGEDAEHVARLADTD EALPPILVERSTLRVLDGMERVLAKKAGHTTIEVRLEDGAERSPLLAVRSNWTHGL PLSRQDRRAAAQRILAQMEHLSDRAVAGIAGIAGHAKTVALRPLAAGFTENPQARRGED PLSRQDRRAAAQRILAQMEHLSDRAVAGIAGIAGHAKTVALRPLAAGFTENPQARRGED GRIRPLDGTTGRRKAAELLAQREQASVREVARHAGISPATASDVRRLASGRS PVPER NTFGARPAGGTGSRATPGGGAAPEPVSVVRPIRPEBSPLVRLLRDPSLRHKESGRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ORF5 (364 aa), lankacidin biosynthesis
similar to AJ277117-5 Gluconobacter oxydans pu
protein (359 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MILLGTAAGGGFPQMNCACALCARGRRGELPARSQECVAVSGDG
RDMMLLNASDIRTQLLAAPALTPGROERDTPVRGVVLIDARVHALGLAVLRGATGL
TVYAAPPVRGALSAELPVRGLLDRYARDMRMADTAPGGFAVAGGLTVTAHPVGTTKPA
YAHAPDPDAPMVCAYRIEDPATGGALVYAPCLATWPDGFDDLLASATCALLDGTFFSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4922. .5812)
/note="ORF4 (296 aa), lankacidin biosynthesi
similar to AE004625-4 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to Y00459-2
                                                                                                                                                                                                                                                                                                                                                                                         /product="pyrroloquinoline
/protein_id="BAC76463.1"
/db_xref="GI:30698350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (5815. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAAVREAGVEVLPDGSELVL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="pyrroloquinoline quinone biosynthesis protein
/protein_id="BAC76462.1"
/db_xref="GI:30698349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyrroloquinoline quinone biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/product="StrR-like_regulatory_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein, StrR (350 aa) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3659. .4645)
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/transl_table=
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/db_xref="GI:30698348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              quinone biosynthesis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          griseus regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is protein
putative pqqB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (304 aa) "
              aa) "
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RESULT 12
AX697993
LOCUS
   DEFINITION
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Best Local Similarity
Matches 401; Conserv
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AX697993
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                               GTGGACCGCCTCACCG
                                                                                                                                                                                                                                                                                                                               CGCCTGGTGCGGGCCGAGGCCGCCGCGGCGGTGCTCGGGCACGCCGGGGCCGGGCCGTCGAC 59766
                                                                                                                                                                                                                                                                                                                                                                                                     TCCCGGCTGCGCGACAAGCTCCTGCCGCTGCCGGCCGGGGAGCGCCGCGAACACCTGCTG 59826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGAGCTGCGGACCACCCTGGACGCCGGGGGACCCCGTGGGTGTGTGGTGGACCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGGCCAGGACTTCCTGCGCCGCCAGGGCATGCGGCCCCTGCCGCCCGAGCAGGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGCGGCGACTACCTGCGCAGCCAGGGGCCTGCGCGCCCATGGACCCGCAGCGGGGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCTGCCCGCGTCGCCTGGGGGCTGTGGGACGGACCGGCATGGCCGGCAC
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                                                                                                                                                                                   CGCATCACCGCGGCGACCGGCCTGCGCGAGGCGACCACCCTGGT
                                                                                                                                                                                                                   CGGCTCGCGGCGTGACCGGGGTCCGGGTGGCCACGACCATCGTCTTCGACCACCCGACA
                                                                                                                                                                                                                                                                                         CGTGACGTCGCCTTCCGTGACCTGGGATTCGACTCCATGACCGCCGTCGACCTGCGGAAC
                                                                                                                                                                                                                                                                                                                                                                 CGGCTGGTCCGAGCCGAGGTGGCAGCGGTGCTGGGCCACGCCACGCCGACGGTGATCGAG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCGTACGCTGCCCGCCGCCGCTCGGCCGGAGAGCCCGCGGAGGAACCCGGAGGGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCGCGCGTTCCTCGACCTCATGGGCGCGCTCCCGGCACCGGCCGCTGTTCGACGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGAGCGGTTCGTCGAACTGTTCACCGCCGCCGCCGCCGGCCCCTCTTCGACGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTCCTACGCGGCGGCAACGCCTTCCTCGACGCCTTCGCCCGTCGTGGTCGGCGCAGT
                                                                                                             GTCACCGCGCTCGCCG
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   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar to AL133424-19 Streptomyces ABC transporter ATP-hinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF8 (34 aa), lankacidin biosynthesis protein similar to AL603642-197 Sinorhizobium meliloti putative protein A (31 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLRLAEAVGLERDEVHDERLVLAGTRFAVDAYYDFARRRPWLEAAASGLTELFSPGLL
AHRLGRLREHYPWIAEEGFBYFTARIEVVGPEGRSLLDLVARHAVSREQQEACVRALA
FKCRVLNAVLDSLDYHTGNGATRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (7926. .8030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="pyrroloquinoline
/protein_id="BAC76466.1"
/db_xref="GI:30698353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABC transporter ATP-binding protein /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="ORF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MRTSGKELPAKKAWHRPDFVTIDTGMEVTAYFSR
   from Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.5%;
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                                                                                                             59630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 243.6; DB 1
Pred. No. 1.5e-16;
 4725 bp
WO03010193
                                                                                                                                                                                                                                                                                                                                                                                                                                         -CGTCGATGCCGGAGGCCGAACGTCACGAGCATGTCGCC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194;
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                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coelicolor putative (544 aa)"
                                                                                                                                                                                   CTTCGACCGGCCCAGT
                    PAT
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                  02-APR-2003
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                                                                                                                                                                                                                                                                                         519
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                                                    RESULT 13
AX697977
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AUTHORS
TITLE
DEFINITION
ACCESSION
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Location/Qualifiers
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LTEADARS PEYWVRHARAAVEFLDGVRLLEDOGGVTTILLELGEDGVUSAMARDCLRDAG
TVCVPLLRGRDRTEPEALLAALAGLYVRGVPWDWERT ATEAGRRVPLPTYA FORRRH
WLPESQASSARRPVNGGGHAGQAGHAGQAGHAGHDGEPAPAVDRTTPELLYR
DRTTLELVRDATAQVLGHAS PDDVATHEAFRELGFSSLMLAELGERLIEATGRRVPT
LLFDHFTFDALARRLEADGARRTDAGPVS PPAAAHHDDPT VI VGMGCRLPGGVRSPE
DLWRFVAAGGDA I SALFVDRGWEFPAADFPGEGGFLANGFPG IS PREALAMDP
QORLLETSWEALERAGVDALKLRGSRTGVFVGASPSEYGPRLHETSDAGGVTVMATS
PSVLSGRI AYVLGLEGPALTVDTACSSSLVALHLAAQALRGGECDLALAGGVTVMATS
GMFAEFFARGGGLAPDGRCKAFADGADGTGWGEGGVGLAVQRUSDAVRDGRPVLAVVRG
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AAVGYVELHGTGTPTGDPVERAAPAI HAGAGREAGQPLLVGSVETVNIGHLEGAAGISA
LLKAVLAVERREIPATLHHASPIPAI IPMAELGIGVNTÄLTFWPEQAGPLVVGVSSEGA
GTNCHVVLTEPAGYDAAAR PATAGIR PAGTPAPLLVSGRDEQALRAQARKLROHLDT
HPGLPLRDVAHTLAAARAPLARRAVLLAADREDVSAGLARLADGTPGADLVRGTVSPG
ALAFVPTGQGSQRPGMTÄELYRTSAEYAAALDEVCASLDRAMLRRPLRDVLFAAGEGSDE
AALIDRTEFTQPALFAVEVALFRYAERIGGLTPRFLICHSVGELAAAHVAGVLSLADAC
TLVAARGRLMQDRPATGAMVSVQATEDELAPPVSESTTLAALNGPASTVIAGDEDAVL
                                                                                                                                     LLGTAGSLSSGVAATAVLVQAWTDLGGGARLWCLTRGAVSVSPSDPLAAPAQAQLWGM
GRVAALEHPERWGGLVDLPAVPDDRAWTRLCAVLAGGSGEDQVAVRAAGLPARRLGRA
GTRADAAPAGPSPWRTDGTVLVTGGTGALGAHLAQWLAAAGAAHVLLTSRRGPDADGA
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LLATYGQDRPDDRPLWLGSVSASIGHTQAAGVSVIKSVLALANGLLEKTLHVDEFT
PEUDWSAGAVELLTEGREWPETDGPRRAGVSAFVGISCTNAHVILEQAESVEEPVTAPA
DDGLLVPWVVSARSBEALRAQARRLADHVRESGLRFADVGLSLAVTRAGLEHRAVLVA
                                            ABLTARLRETGTEVTVAACDVTDRDALABLLSGLPADRPLTGVVHAAGVLDDGVLDSL
TPDRPAAVAGPKVTGAWHLHBLTRDLDLSAFVLFSSFAGTVGLAGQANYAAANAYLDA
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GPDGTLTTLAHDTAHDAGRDVAAVPALRGDQPETRTVVTAVGRLYATGLTVDWPAFFA
PYGARPTELPTYAFQHRRYWLEPVAPSSAPPANPLRYRTAWASVPDGPRPSLSGTWAV
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EVCAAFDGLLPGALREVVFGGAGLDRTEWAQPALFALEVALFELVSSWGVRADVLLGH
SIGELAAAYVAGVWSLADACRIVAARGRLMQALPEGGAMVAVEAAEDELPDLPGGVSV
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VDBFDAGFFGISPREAAAMDPQQRIVILELSWEALBEDAGIFPARLGGSGAGVFVGAIAD
DYAFILSRAAGADAATPQTTTGLINGGIIANKYSYTLGILGFSFFVDSGQSSSLVAVHLA
ABSLRRGECSVALAGGVNLIILAEDSTVAVERFGALSPDGYCYTFDARANGYVRGEGGG
LAVHRAQLGLPATAVAWGSWSGAGMAADTEAARRQLARTGLVPLAPDAALAALGQVMD
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